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THE DESIGN AND ANALYSIS OF SALMONID TAGGING STUDIES IN THE COLUMBIA BASIN

Volume V: Analysis of In-River Growth
for PIT-Tagged Spring Chinook Smolt

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THE DESIGN AND ANALYSIS OF SALMONID TAGGING STUDIES IN THE COLUMBIA BASIN

VOLUME V

Analysis of In-River Growth for PIT-Tagged Spring Chinook Smolt

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PREFACE

Project 8910700, Epidemiological Survival Methods, was developed to provide statistical guidance on design and analysis of PIT-tag (Passive Integrated Transponder) survival studies to the Northwest fisheries community. Studies under this project have determined the statistical feasibility of conducting PIT-tag smolt survival studies, assessed analytical capabilities for analyzing the tagging experiments, and made recommendations on study design. As PIT-tag capabilities developed and research interests increased, the project has been instrumental in maintaining the statistical capabilities for designing and analyzing tagging studies to meet these expanded objectives.

Given that the lengths of tagged fish have been often measured at the release site, and at least at one downstream detection site for many PIT-tag releases, it is possible to study the growth of particular salmonid species, runs, year-classes, and reared types, during their downstream migration. In general, in the absence of age information, fish growth can be assessed by means of the relationship between the release and recovery sizes of tagged fish. The purpose of this report is to present an approach to analyze the in-river growth of PIT-tagged salmonid yearlings. We illustrate the use of Walford's lines, Kolmogorov-Smirnov tests and one-tail paired t-tests to detect in-river growth for samples of PIT-tagged fish, and provide a simple three-step protocol to select adequate data for an unbiased analysis. Finally, we illustrate the between-sample comparison of growth rates by means of a simple linear model.

ABSTRACT

The length of tagged fish is often measured at the release site and at least one downstream detection site for many PIT-tagged releases, enabling the study of growth of a particular salmonid species, run, year-class and rearing type, during their downstream migration. The purpose of this report is to suggest an approach to analyze the in-river growth of PIT-tagged salmonid yearlings.

Since the age of the tagged fish is unknown, its growth must be assessed by means of the relationships between the release and recovery sizes of tagged fish, and between those and the time elapsed between release and recovery. Analyses of this type require adequate samples. A simple three-step protocol for selecting adequate data for unbiased samples is provided.

Three methods: Walford's lines, Kolmogorov-Smirnov tests and one-tail paired t-tests, are suggested as analytical tools and applied to detect in-river growth from selected samples of PIT-tagged spring chinook yearlings. Finally, the between-sample comparison of growth rates by means of a simple linear model is discussed.

EXECUTIVE SUMMARY

Objectives

In this report we illustrate the use of Walford's lines, Kolmogorov-Smirnov tests and one-tail paired t-tests to detect in-river growth for samples of PIT-tagged fish, and present a simple linear model that allows the statistical comparison of growth rates between samples.

Results

The application of Walford's lines, Kolmogorov-Smirnov tests and one-tail paired t-tests to two samples of PIT-tagged spring chinook, one of hatchery-reared releases and one of wild releases, have shown the occurrence of in-river growth in both cases. The hatchery fish grew on average some 6 mm over a period of around 10 days, while the wild fish grew some 33 mm during an average migration time of 43 days. However, the rather strict condition of a constant travel time within a sample, that the three methods impose to avoid biased estimation, prevented a statistically formal, direct comparison of growth between the two samples. To make possible a comparison of sorts, we defined individual growth rates (\hat{G}) as the difference between the observed lengths at release and recovery, divided by the travel time of each fish in the samples and fitted a linear model with three predictor variables: the release day (D), the length at release, and the fish average speed (S), calculated as the distance traveled over the individual travel times. After a series of F-ratio tests, we determined that the wild and hatchery fish of our examples grew at different rates: $\hat{G} = 0.240 + 0.005D$ for the wild fish, and $\hat{G} = -2.723 + 0.026D + 0.035S$ for the hatchery fish.

Management implications

Walford's lines, Kolmogorov-Smirnov tests, and one-tail paired t-tests can assess in-river growth in samples of PIT-tagged fish. However, the methods differ in their approaches. The Kolmogorov-Smirnov test detects growth if the hypothesis that the distributions of release and recovery lengths of the tagged fish are equal is rejected at a given α level. The t-test assumes that the difference between recovery and release lengths d_i is normally distributed. When the

hypothesis that $d_i \leq 0$ is rejected, the growth between release and detection times is confirmed. Walford's lines express growth as a linear relationship between recovery and release lengths. Growth between release and detection times is confirmed when the hypothesis that the line is equal to the line $\hat{L}_{recovery} = 0 + 1 \times L_{release}$ is rejected.

The three methods require that the lengths at time of release and recovery of the individual fish in the sample be measured over similar periods (travel times) to avoid biased estimates. Samples of PIT-tagged fish for an adequate analysis of in-river growth may be identified by following a three-step protocol: identification of reaches with large sample size, inspection of travel-time distributions, and assessment of the relationship between travel time and release length.

Recommendations

Until PIT-tag experiments designed to assess growth under particular circumstances are performed, Walford's lines, Kolmogorov-Smirnov tests or one-tail paired t-tests may be applied to samples from the current PIT-tag data base. However, these samples should not be selected solely on the basis of the particular criterion of interest (e.g., reared type, time and locale of migration, size at release, site of origin, etc.). Careful attention must be paid to the inspection of the travel-time distribution and the correlation between travel time and release length of each potential sample to avoid bias in the analysis of growth. Once that growth has been detected for a sufficient number of adequately selected samples, linear modeling may eventually be used to compare growth rates.

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1. INTRODUCTION

Fish growth, the increase or progressive development of fish, is a very complex process. However, it can be measured by assessing the change in length or weight of an individual fish or a group of fish between two sampling times. When both the size and age of individual fish are known, the assessment of fish growth involves the study of the average size of the fish at each age (i.e., absolute growth) or of the gain in size for some fixed and short period of time in relation to the size at the beginning of the period (i.e., relative growth) as a function of age. In the absence of age information, fish growth can be assessed by means of the relationship between the release and recovery sizes of tagged fish (Ricker 1975, pp. 228-230).

Since 1988, hatchery and wild salmonid species have been PIT-tagged under programs conducted by the National Marine Fisheries Service, Idaho Department of Fish and Game, Oregon Department of Fish and Game, and the U.S. Fish and Wildlife Service. Often the length of tagged fish was measured at the release site, and at one or more downstream detection sites. In the absence of age information, these lengths are adequate for the study of the growth of particular salmonid species, runs, year-classes, and reared types during their downstream migration over selected reaches.

The purpose of this report is to present an approach to analyze the in-river growth of PIT-tagged fish. Three simple methods (Walford's lines, Kolmogorov-Smirnov test, and t-test) may be used in the analysis after careful data selection. After these methods have shown in-river growth for various samples of PIT-tagged fish, simple linear regression and analysis of covariance techniques can be used to compare the samples. The procedures are illustrated with two examples.

2. MATERIALS

In order to assess the in-river growth of PIT-tagged salmonids for a particular group of fish (e.g., spring hatchery chinook migrating downstream between Lower Granite Dam and Lower Monumental Dam), careful data selection must precede the analysis of growth. The objective of such selection is to obtain an adequate sample size of PIT-tagged fish of representative size classes. For example, fish in the sample should be of about the same age, release-length, and origin; and they must travel along the reach in about the same time. Achieving all of these criteria may be difficult, because either the information is not available (e.g., age, origin, or birthplace) or some sampled fish may move downstream in erratic ways, spending more time in their migration than other fish of the same cohort. In following paragraphs, we describe a three-step protocol that may help to identify an adequate sample for the analysis of in-river growth.

2.1 Identification of Sampling Efforts

Information on the PIT-tag numbered fish, release and recovery sites, dates and lengths for tagged fish of a particular species, run, year-class and reared type can be obtained from the Columbia River Data Access in Real Time (DART) database. Sample sizes of cohorts of juveniles for potential analysis of within-reach in-river growth are summarized in Tables 1-2, for hatchery and wild spring chinook of the 1994 year-class, respectively. The first columns of these tables indicate the release sites, and the first rows, the recovery sites. The length, and often the weight, of the PIT-tagged fish were measured at both sites. It is clear from these examples that a considerable variability in sample size may be expected among reaches and between rear types, thus limiting the scope of growth-related question that may be investigated with the PIT-tag database. Groups with sample sizes of more than 30 fish are desirable, and a quick inspection of Tables 1-2 can help to identify possible sets of fish for a subsequent growth study. The larger the sample size, the better, because it is quite likely that additional fish will be discarded before analysis can be performed. For example, the reaches Dworshak - Lower Monumental Dam (DWOR-LMN), Lower Granite Dam - Lower Monumental Dam (LGR-LMN), Little Goose Dam - Lower Monumental Dam (LGS-LMN), and Dworshak - Clearwater Traps (DWOR- CLWTRP),

Table 1: Number of PIT-tagged hatchery spring chinook, year-class 1994, whose lengths were measured both at the release and recovery locations. Top row indicates recovery-location or lower-reach boundary, first column indicates release points or upper reach boundary. See Appendix for location names.

Upper	Lower Reach Boundary			JDA	LGR	LGS	LMN	REDTRP	RIS	SALTRP	SAWTRP	SNKTRP
	CLWTRP	GRANDR	IMNTRP									
BIGFLC	0	0	0	0	0	0	2	0	0	0	0	0
CROTRP	2	0	0	2	5	2	5	0	0	0	0	0
DWOR	1	0	0	19	10	35	90	0	0	0	0	1
ENTH	0	0	0	0	0	0	0	0	1	0	0	0
GRANDR	0	0	0	0	0	1	6	0	0	0	0	0
IMNAHW	0	0	48	3	1	1	18	0	0	0	0	1
KOOS	0	0	0	0	0	1	1	0	0	0	0	0
LEAV	0	0	0	2	0	0	0	0	0	0	0	0
LGR	0	0	0	10	0	14	373	0	0	0	0	0
LGS	0	0	0	17	0	0	423	0	0	0	0	0
LMN	0	0	0	28	0	0	0	0	0	0	0	0
LOOH	0	3	0	1	1	1	26	0	0	0	0	0
PAPOOC	0	0	0	1	0	0	1	0	0	0	0	0
PETKEC	0	0	0	0	4	0	4	0	0	0	0	0
POWP	3	0	0	0	2	0	11	0	0	0	0	0
RAPH	0	0	0	2	0	1	9	0	0	5	0	4
REDP	0	0	0	0	1	0	0	2	0	0	0	0
SALR	0	0	0	0	0	0	1	0	0	1	9	0
SAWT	0	0	0	1	0	0	3	0	0	1	0	0
SNAKER	0	0	0	19	9	8	120	0	0	0	0	0
SQUAWC	0	0	0	0	3	0	0	0	0	0	0	0
WHITSC	0	0	0	0	4	0	0	0	0	0	0	0
WINT	0	0	0	0	0	0	0	0	2	0	0	0

Table 2: Number of PIT-tagged wild spring chinook, year-class 1994, whose lengths were measured both at the release and recovery locations. Top row indicates recovery-location or lower-reach boundary, first column indicates release points or upper reach boundary. See Appendix for location names.

Upper	Lower Reach Boundary														
	CLWTRP	CROTRP	GRANDR	JDA	LGR	LGS	LMN	MARSHC	MARTRP	MCN	REDTRP	SALR	SALTRP	SAWTRP	SNKTRP
BEARVC	0	0	0	0	1	0	1	0	0	0	0	0	3	0	1
BIGC	0	0	0	0	6	0	3	0	0	0	0	0	2	0	0
CAMASC	0	0	0	1	2	0	1	0	0	0	0	0	0	0	0
CATHEC	0	0	20	0	2	0	1	0	0	0	0	0	0	0	0
CFCTRP	2	0	0	0	17	0	0	0	0	0	0	0	0	0	0
CHAMWF	0	0	0	0	4	0	1	0	0	0	0	0	0	0	0
CLEARC	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0
CROOKC	0	0	0	0	22	0	4	0	0	0	0	0	0	0	0
CROOKR	0	75	0	0	20	0	0	0	0	0	0	0	0	0	0
CROTRP	3	0	0	1	86	0	0	0	0	0	0	0	0	0	0
ELKC	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
FRENCC	0	0	0	0	2	0	0	0	0	0	0	0	1	1	0
GRANDR	0	0	0	2	43	0	7	0	0	0	0	0	0	0	2
HERDC	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
LAKEC	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0
LEMHIW	0	0	0	0	1	0	6	0	0	0	0	0	0	0	1
LOLOC	4	0	0	1	4	1	9	0	0	0	0	0	0	0	1

Table 2: (Continued)

Upper	Lower Reach Boundary														
	CLWTRP	CROTRP	GRANDR	JDA	LGR	LGS	LMN	MARSHC	MARTRP	MCN	REDTRP	SALR	SALTRP	SAWTRP	SNKTRP
LOOKGC	0	0	3	1	1	0	7	0	0	0	0	0	0	0	1
MARTRP	1	0	0	0	14	1	12	3	0	3	0	0	12	0	4
MINAMR	0	0	1	0	2	0	5	0	0	0	0	0	0	0	1
NEWSOC	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
REDR	1	0	0	1	16	0	2	0	0	0	31	0	0	0	0
REDTRP	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0
SALR	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0
SALREF	0	0	0	0	0	1	2	0	0	0	0	1	1	0	0
SALRNF	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
SAWTRP	0	0	0	0	3	1	0	0	0	0	0	0	1	0	0
SECESR	0	0	0	0	3	0	2	0	0	0	0	0	0	0	0
SMILEC	0	0	0	0	7	0	0	0	0	0	0	0	0	3	0
SNAKER	0	0	0	0	0	0	14	0	0	0	0	0	0	0	0
VALEYC	0	0	0	0	0	0	2	0	0	0	0	0	1	0	1
WENRSF	0	0	1	0	0	0	4	0	0	0	0	0	0	0	0

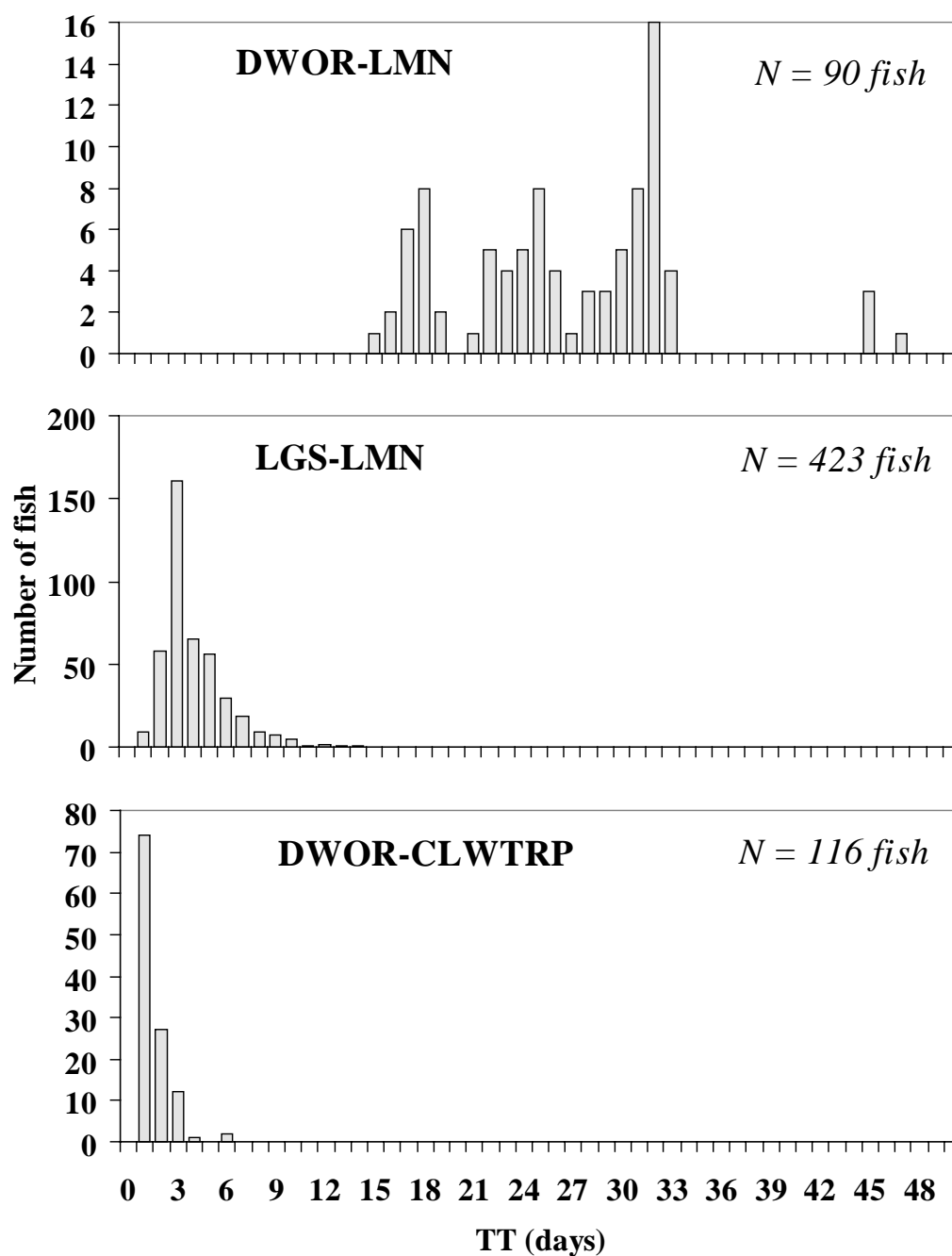
with sample sizes of 90, 373, 423 and 116 fish, respectively, appear as good candidates for the study of the in-river growth of spring hatchery chinook (Table 1). For spring wild chinook (Table 2), good options are less abundant. Only three reaches had adequate sample sizes: Crooked River - Crooked River Traps (CROOKR-CROTRP) with 75 fish, Crooked River - Lower Granite Dam (CROTRP-LGR) with 86 fish, and Grande Ronde River - Lower Granite Dam (GRANDR-LGR) with 43 fish. The comparison of both tables, on the other hand, indicates that the assessment of growth differences between wild and hatchery at a given reach, is not possible for the 1994 spring chinook, because there was little correspondence between the reaches intensively sampled for both types of fish.

2.2 Inspection of Travel-Time Distributions

After selecting groups of PIT-tagged fish for analysis, it is convenient to characterize distributions of travel times (Fig. 1). Travel time is defined as the difference between release and recovery dates expressed in days. The inspection of these distributions may suggest how homogeneous are the travel times. Homogeneous samples are required to guarantee an accurate measure of growth for a given fish group (e.g., 1994 hatchery spring chinook migrating from LGR to LMN). In general, relatively narrow distributions, with well-defined modes, indicate samples that are more homogeneous. Widely dispersed and polymodal distributions suggest more heterogeneous travel times.

Figure 1 shows three examples for hatchery spring chinook. The travel time distributions for smolt in the reaches LGS-LMN and DWOR-CLWTRP are narrow and clearly unimodal. This suggests that most tagged fish were probably of about the same age and origin. Moreover, because both reaches are relatively short (46 and 55 km for LGS-LMN and DWOR-CLWTRP, respectively), the differences in travel times within each group reflect random variation or mild heterogeneity among individuals. On the other hand, the diffuse and polymodal distribution for DWOR-LMN suggests that at least three different groups of fish may have been present in the sample. In the absence of information on the age of release and the origin of the fish, one cannot be totally sure whether the three modes truly represent distinct groups of fish, or just an artifact of

Figure 1: Examples of distributions of travel time (TT) for hatchery spring chinook, year-class 1994 over three reaches: Dworshak - Lower Monumental Dam (DWOR-LMN), Little Goose Dam - Lower Monumental Dam (LGS-LMN) and Dworshak - Clearwater Traps (DWOR-CLWTRP). N indicates sample size.



a small sample size combined with a very large reach. The distance between DWOR and LMN is 222 km, and the sample only had 90 fish.

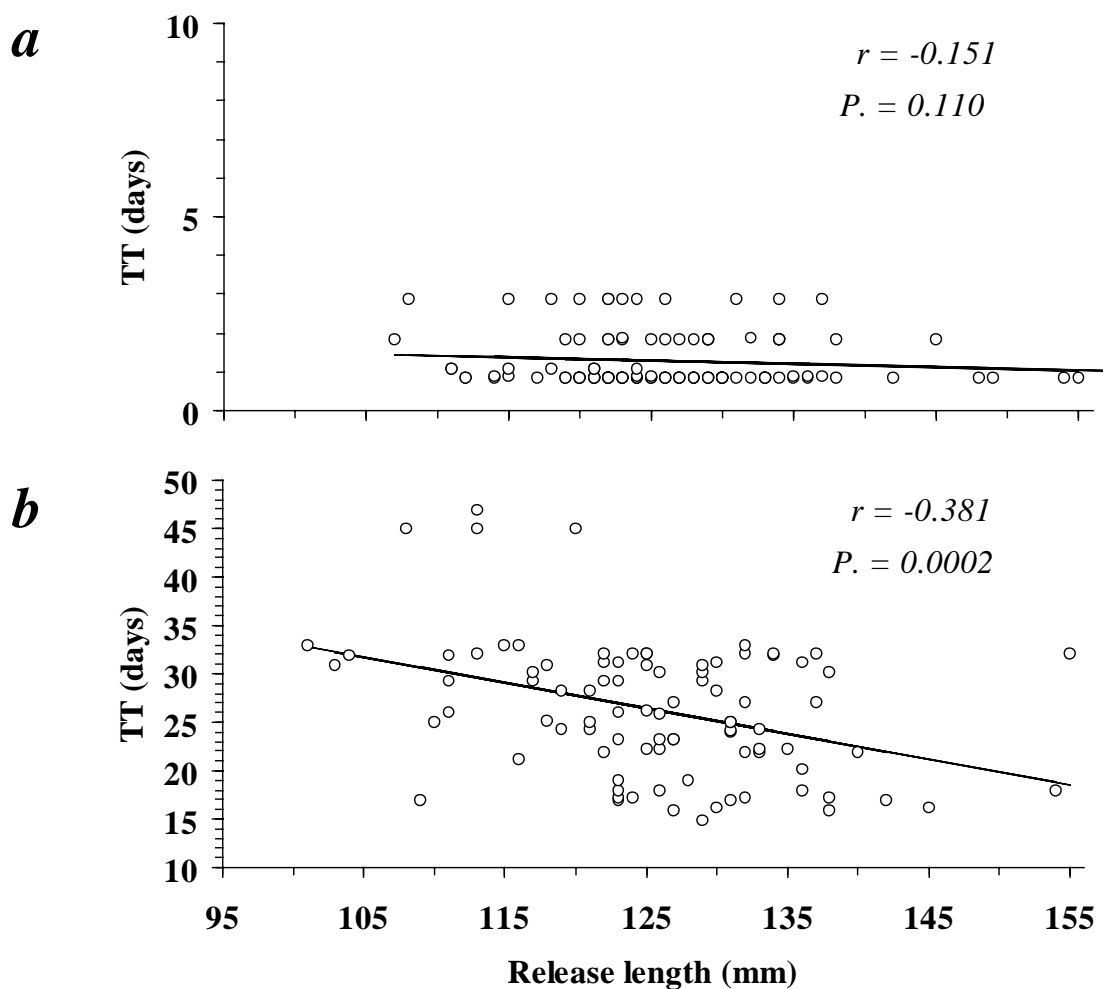
2.3 Relationship between Travel Time and Release Length

In the absence of age information, large sample sizes and homogeneous samples are not sufficient requirements for accurate measures of growth of particular groups of tagged fish. In such cases, not only the lengths of release and recovery must be known for all the fish in the sample, but also the period between release and recovery (i.e., travel time) must be about the same for all the fish. In 1994, these data requirements are not realized.

All the fish in the sample, both large and small, may be assumed to have the same opportunity to grow during their downstream migration (i.e., travel time remained about constant), if a potential sample of tagged fish does not show a significant negative correlation between travel time and release length, and the range of travel times is not large (Fig. 2a). For the example depicted in Figure 2a, for instance, one can assume that the 116 fish migrated between Dworshak and Clearwater traps in about 1.3 days, both the smaller fish (105-115 mm) and the larger fish (135-155 mm) having about the same opportunity to grow. In this situation, the use of the whole sample in the subsequent analysis will probably not bias the assessment of growth.

On the other hand, when a potential sample of tagged fish shows a significant negative correlation between travel time and release length, and the range of travel times is large (Fig. 2b), large fish, traveling faster than small fish, are likely to have less time to grow than the small fish. Thus, for the growth analysis, it cannot be assumed that the lengths of release and recovery were measured over a constant period. In this situation, the use of the whole sample would inaccurately measure growth. However, if the original sample size is large enough, smaller subsets could be identified (e.g., modal classes for the original distribution of travel times) and used in the analysis of growth.

Figure 2: Examples of relationships between travel time (TT) and length of release for hatchery spring chinook, year-class 1994: (**a**) 116 fish of the Dworshak - Clearwater Traps (DWOR-CLWTRP) sample showing lack of correlation, (**b**) 90 fish of the Dworshak - Lower Monumental Dam (DWOR-LMN) sample showing a significant negative correlation.



3. ANALYSIS OF GROWTH

Once an adequate sample has been identified, there are three common approaches to analyzing growth data. The three methods rely on measures of lengths at release and recovery assuming a constant travel time for all fish. All three methods require sample sizes of at least 30 fish.

3.1 Walford's Lines

Walford's lines have long been used in fisheries biology as a simple graphical approach to determine growth (Walford 1946). The original idea consists of plotting the lengths at age $t+1$ against the lengths at age t . The slope of the resulting line is equal to k (Ford's growth coefficient which is equal to e^{-K}), and the intercept is equal to $L_{\infty}(1-k)$, from which von Bertalanffy's asymptotic length L_{∞} can be calculated.

For tagged fish, the method consists of plotting the length at release on the x -axis and the length at recovery on the y -axis. Recoveries must occur after a more or less constant period. In classical studies, this period is of one or more years (e.g., Ricker 1975, pp. 223-224). In our case, the travel-time class we chose determined the period, measured in days; thus, the analysis measured seasonal growth rates. Formally, Walford's model can be written as:

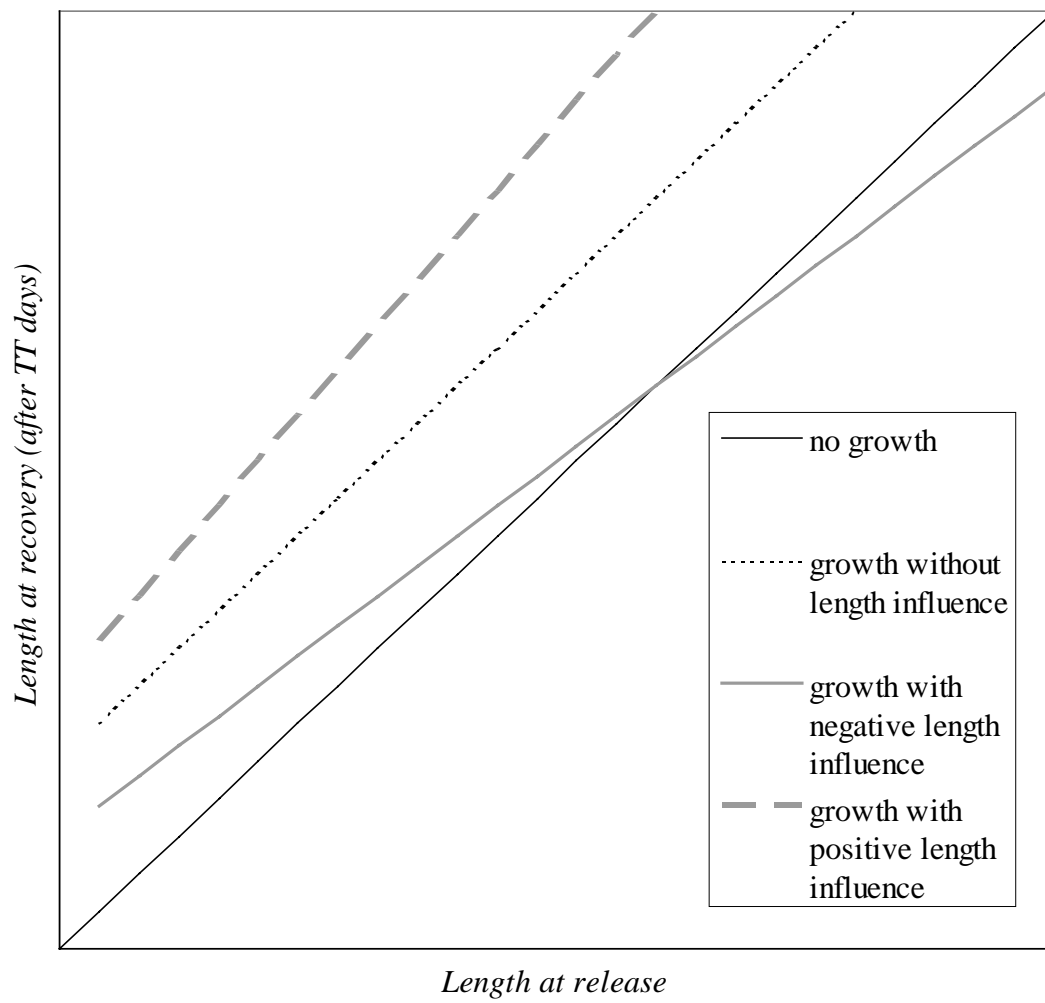
$$L_{recovery} = \alpha + k \cdot L_{release} + \varepsilon, \quad (1)$$

where L is the measured length and the error term ε is assumed to be distributed as a standard normal deviate [i.e., $N(0, \sigma^2)$].

There are three possible outcomes (Fig. 3) in plotting the data:

- (a) Data points lie on the $x = y$ line, indicating no significant growth.
- (b) Data points lie on a line parallel to the $x = y$ line, which indicates growth but no influence of release length.
- (c) Points lie on a line not parallel to the $x = y$ line, which indicates growth and influence of release length on growth.

Figure 3: Hypothetical Walford's lines.



If the slope of the line is less than 1, larger fish grew less than smaller fish. If the slope is greater than 1, larger fish grew more than smaller fish.

For a given subset of the data, we can estimate the Walford's line using straight-line regression, and determine if the regression line is significantly ($\alpha = 0.05$) different from the $x = y$ line of no growth.

3.2 Comparison of the Length Distributions for Released and Recovered Fish: Kolmogorov-Smirnov Test

For the selected subset of fish in the analysis, the length distributions of released and recovered fish can be directly compared by means of the Kolmogorov-Smirnov test. The null hypothesis to be tested is that both length samples have the same distribution. If the null hypothesis is rejected, we may attribute the difference to growth.

For the Kolmogorov-Smirnov test, the cumulative relative frequencies are calculated for both samples as:

$$\text{rel } F_{ij} = \frac{F_{ij}}{n}, \quad (2)$$

where n is the number of length measurements taken and F_{ij} is the number of length measurements $\leq L_i$ in sample j (the released or recovered fish). The Kolmogorov-Smirnov test statistic Kolmogorov 1933, Smirnov 1939) is:

$$D = \max \left[\left(\max D_i \right), \left(\max D_i' \right) \right] \quad (3)$$

where

$$D_i = \left| \text{rel } F_{i,\text{release}} - \text{rel } F_{i,\text{recovery}} \right| \quad (4)$$

and

$$D_i' = \left| \text{rel } F_{i-1, \text{release}} - \text{rel } F_{i, \text{recovery}} \right|. \quad (5)$$

Critical values for this test statistic $(D_{\alpha, n})$ are found in tables (e.g., Table B9 in Zar 1984, pp. 546-548). If $D \geq D_{\alpha, n}$, the null hypothesis is rejected at the α level of significance, and growth may be inferred.

3.3 Comparison of the Mean Lengths of Released and Recovered Fish: t-Test

Providing that the length distributions for released and recovered fish have a reasonable sample size ($n \geq 30$), we can use one-tail paired t-tests. The null hypothesis will be that $(\bar{L}_{\text{recovery}} - \bar{L}_{\text{release}}) \leq 0$, where \bar{L} represents the mean lengths. Rejection of the hypothesis (e.g., at $\alpha = 0.05$) will imply that growth occurred during the travel time. Paired t-tests are better than Kolmogorov-Smirnov tests to show growth.

3.4 Comparison of Growth between Samples

The previous three methods are appropriate to assess growth for tagged fish in a given sample. However, they may present a serious drawback if one wants to use them to compare growth between samples coming from different reaches and/or consisting of different type of fish (e.g., hatchery vs. wild chinook). The three methods compare the distribution of the lengths measured at the release site with that of the lengths at the recovery site. Given that there is no information on the age of the tagged fish, the sample is required to comply with the condition of a constant time (i.e., travel time TT) between the first and last length measurements to avoid bias in the estimation of growth. This strict prerequisite may determine a considerable reduction in the number of tagged fish that can actually be used in the analysis of growth for a given reach. Moreover, it will more likely preclude any direct comparison between samples coming from different reaches because it is unlikely that two samples from different reaches will have at least 30 fish each measured over the same time TT . However, once the previous methods have been successfully used to show in-river growth for a few samples, the samples can be compared by redefining the response variable to free the samples from the constant travel time requisite.

The response variable for the Walford's lines, Kolmogorov-Smirnov tests, and t-tests is the length measured after a constant time ($L_{recovery}$) from a first measurement ($L_{release}$). Instead,

one can define the response variable as the growth rate: $G_i = \frac{(L_{recovery} - L_{release})_i}{TT_i}$. This new variable allows the comparison of growth between samples because it does not require a constant travel time. Moreover, by modeling this new variable as a simple linear model of variables such as the date and size of release, and/or the traveling speed, their effect on growth-rate can be analyzed.

For example, let us assume that there are two samples of PIT-tagged fish coming from two different reaches A and B, for which the lengths of 30 or more fish have been measured at both the lower and upper boundaries of the reaches ($L_{release}$ and $L_{recovery}$, respectively). Moreover, let us further suppose that by means of either the Walford's lines, the Kolmogorov-Smirnov test, or the t-test, growth was shown to have occurred at both reaches. Then, we can model growth rate as:

$$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_4 L_{release} + \alpha_5 L_{release} I + \alpha_6 S + \alpha_7 SI, \quad (6)$$

where I is an indicator variable that takes value 0 if the sampled fish came from reach A, and 1 if it came from reach B. Variable D is the day when the tagged fish was released at the lower reach boundary, expressed as a number ranging from 1 to 365. Finally, S is the fish speed, normally expressed in km/day, and measured as $S = \frac{d}{TT}$, with d equal to the distance between the release and recovery sites of the corresponding reach. TT is the fish travel time, normally measured in days. The value of TT is not constrained by the constancy assumption, thus allowing the analysis of all the measured tagged fish in the samples, both "slow" and "fast" fish.

Common regression (e.g., F-ratio tests) and analysis of covariance techniques can be applied to the fit of model (6) to test for significant effects and compare the growth characteristics of each sampling site.

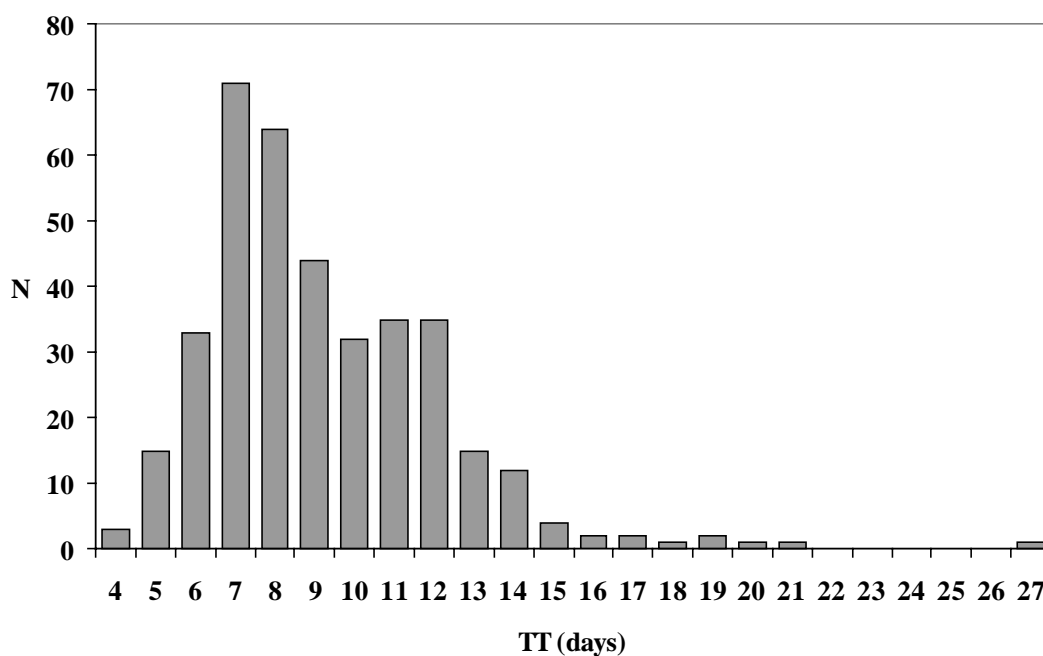
4. EXAMPLES

4.1 Example 1

Our first example corresponds to 373 hatchery spring chinook smolt, year-class 1994, that traveled 106 km from Lower Granite Dam (LGR) to Lower Monumental Dam (LMN). The sample for this reach was the second largest in 1994 (Table 1). The distribution of travel times for the 373 sampled fish was clearly unimodal (Fig. 4), suggesting an homogeneous sample. We started by regressing travel time on length at release to detect any significant length effect which could have confounded our analysis of growth. The linear relationship (Fig. 5) was clearly not significant ($P. = 0.507$); thus, we assumed that all fish in the sample may have had the same opportunity to grow during the average 9.86 days of their downstream migration. We estimated Walford's line from the 373 sampled fish (Table 3). The lengths of recovery were linearly related with the length of release (P-value $\lll 0.05$). The estimated slope was very close to 1, 95% confidence interval = (0.953, 1.011). The tests performed showed that a Walford's line with slope equal to 1 cannot be rejected (P-value = 0.225), but that the line of no growth (intercept = 0, slope = 1) must be rejected. Thus, a new Walford's line, $L_{recovery} = 6.7(\text{mm}) + L_{release}$, was estimated from the data (Fig. 6).

Given that the distribution of travel times was right-skewed, and that travel times ranged from 4 to 27 days, we repeated the previous analysis for smaller subsets with more homogeneous distributions of travel times. Table 4 shows the regression analysis for a Walford's line based on all the tagged fished whose travel times were between the 25 and 75 percentile. The resulting line (Fig. 7) was very similar to the one obtained with the entire sample. When the analysis was repeated for the modal travel-time class, i.e., the class at which most of the travel-time measurements occurred (Table 5), the resulting Walford's line was $L_{recovery} = 5.9(\text{mm}) + L_{release}$ (Fig. 8). Thus, from the Walford's line analyses, we may conclude that the fish grew around 6 mm during their migration from LGR to LMN ($\overline{TT} = 10$ days), what suggests an approximate growth rate of 0.6 mm/day ($\frac{\overline{\Delta L}}{\overline{TT}} = \frac{6}{10}$).

Figure 4: Distribution of travel times for hatchery spring chinook, year-class 1994, in the Lower Granite - Lower Monumental (LGR-LMN) reach.



<i>MEAN</i>	9.86
<i>STD. DEV.</i>	2.91
<i>MODE</i>	7
<i>MEDIAN</i>	9.37
<i>25 PERCENTILE</i>	7.61
<i>75 PERCENTILE</i>	11.7

Figure 5: Relationship between travel time and release length for hatchery spring chinook, year-class 1994, in the Lower Granite - Lower Monumental (LGR-LMN) reach (all travel times included).

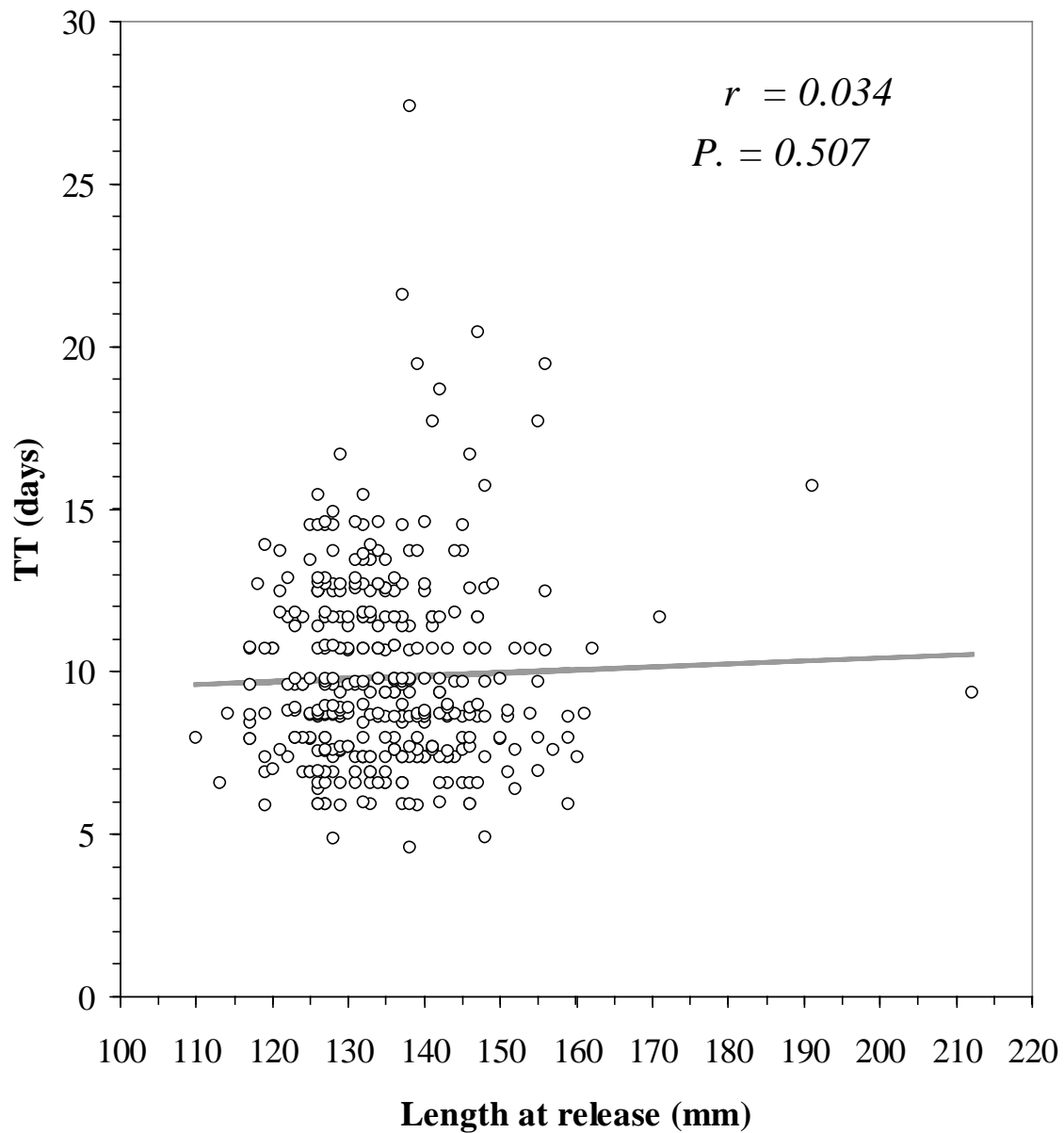


Table 3: Walford's line for 373 PIT-tagged hatchery spring chinook (all travel times included), measured in the LGR-LMN reach, in 1994. **(a)** ANOVA table, **(b)** coefficient of determination (r^2), regression coefficients, standard errors (SE) and 95% confidence intervals, and **(c)** F-ratio test for model $L_{recovery} = \alpha + L_{release}$ (growth without effect of length at release).

(a)

	df	SS	MS	F	P-value
Regression	1	41685.15	41685.15	4427.75	2.535E-208
Residual	371	3492.79	9.42		
Total	372	45177.94			

(b)

$$r^2 = 0.9227$$

	Coefficients	SE	Lower 95%	Upper 95%
α Intercept	9.102	1.998	5.173	13.031
k Slope	0.982	0.015	0.953	1.011

(c)

H_o	Residual SS	df	F	$P.$
$k = 1$	3506.67	372	$\frac{(3506.67 - 3492.79)}{9.42} = 1.475$	0.2254

Figure 6: Walford's line for 373 PIT-tagged hatchery spring chinook (all travel times included), measured in the LGR-LMN reach, in 1994.

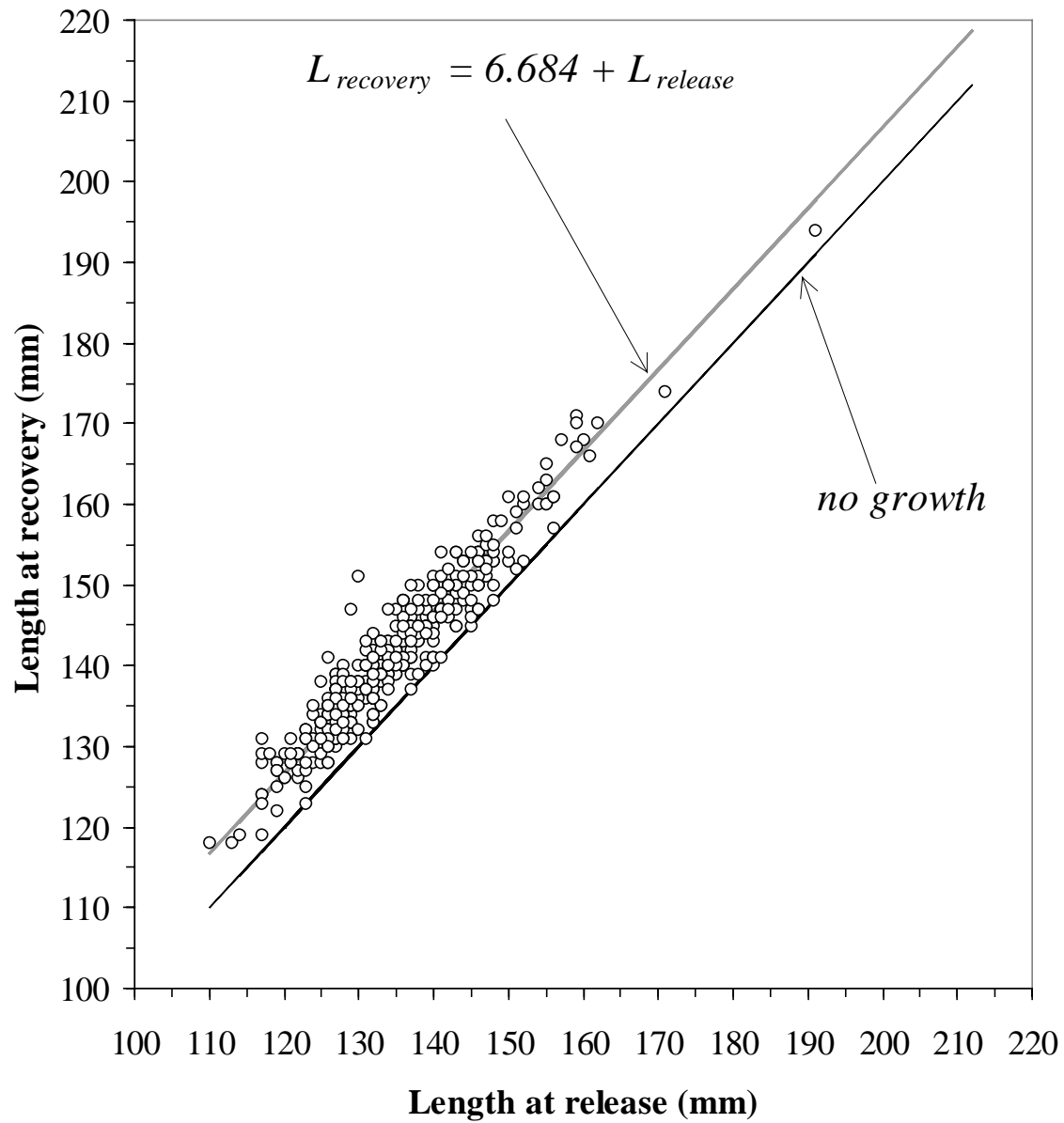


Table 4: Walford's line for a sub-sample of 233 fish (travel times between 25% and 75%) from a sample of 373 PIT-tagged hatchery spring chinook, measured in the LGR-LMN reach, in 1994.

a) ANOVA table, **b)** Coefficient of determination (r^2), regression coefficients, standard errors (SE) and 95% confidence intervals, and **c)** F-ratio test for model $L_{recovery} = \alpha + L_{release}$ (growth without effect of length at release).

a)

	<i>df</i>	SS	MS	F	P-value
Regression	1	28688.87	28688.87	2921.75	4.311E-133
Residual	231	2268.21	9.82		
Total	232	30957.08			

b)

	r^2	0.9267		
	Coefficients	SE	Lower 95%	Upper 95%
α Intercept	6.399	2.509	1.455	11.343
k Slope	1.001	0.019	0.965	1.038

c)

H_o	Residual SS	<i>df</i>	F	$P.$
$k = 1$	2268.27	232	$\frac{(2268.27 - 2268.21)}{9.82} = 0.006$	0.9385

Figure 7: Walford's line for a sub-sample of 233 fish (travel times between 25% and 75%) from a sample of 373 PIT-tagged hatchery spring chinook, measured in the LGR-LMN reach, in 1994.

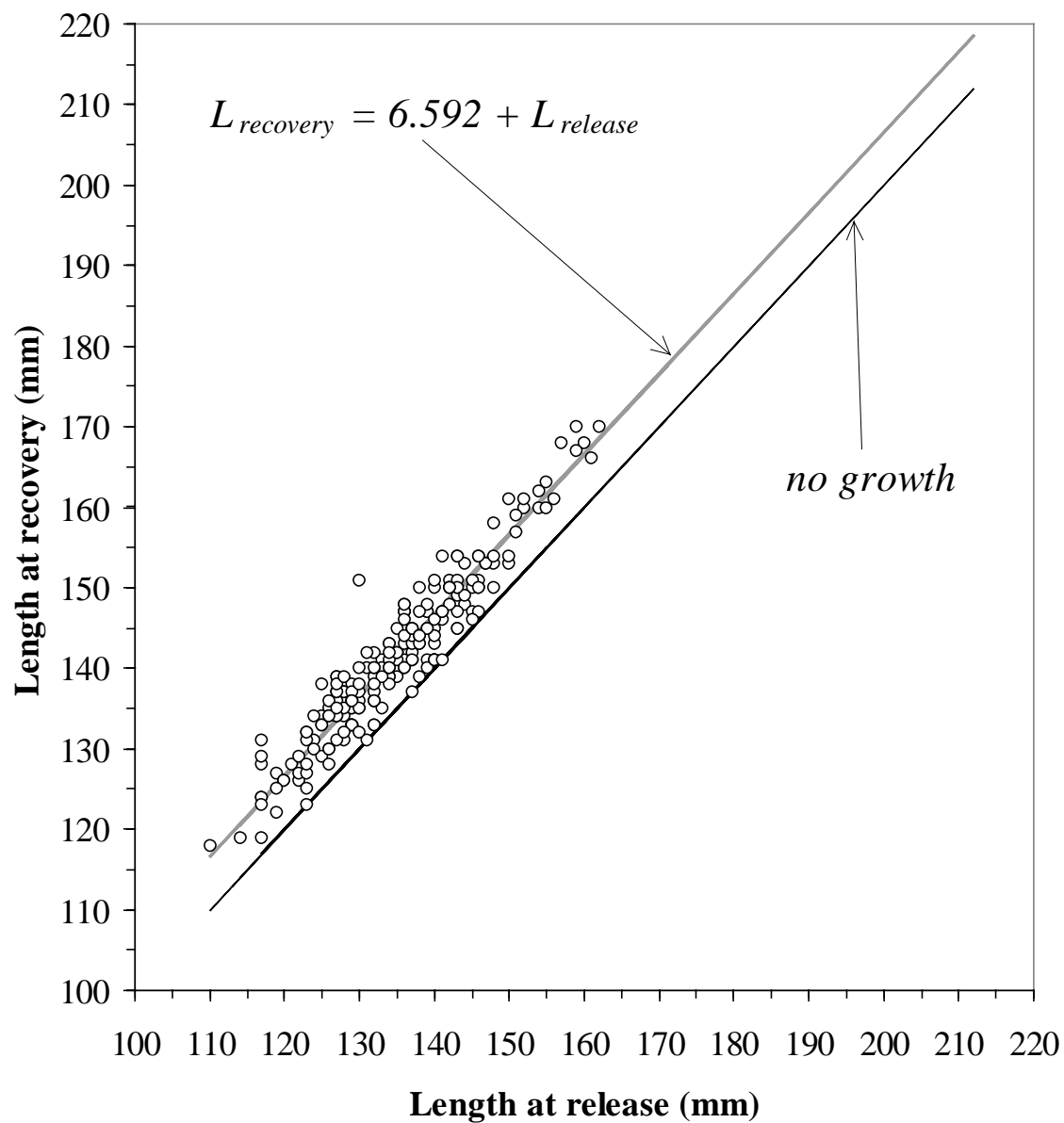


Table 5: Walford's line for a sub-sample of 71 fish (mode of travel times $7 \leq TT < 8$ days) from a sample of 373 PIT-tagged hatchery spring chinook, measured in the LGR-LMN reach, in 1994. **a)** ANOVA table, **b)** Coefficient of determination (r^2), regression coefficients, standard errors (SE) and 95% confidence intervals, and **c)** F-ratio test for model $L_{recovery} = \alpha + L_{release}$ (growth without effect of length at release).

a)

	<i>df</i>	SS	MS	F	P-value
Regression	1	6894.81	6894.812	673.528	2.5246E-37
Residual	69	706.34	10.237		
Total	70	7601.16			

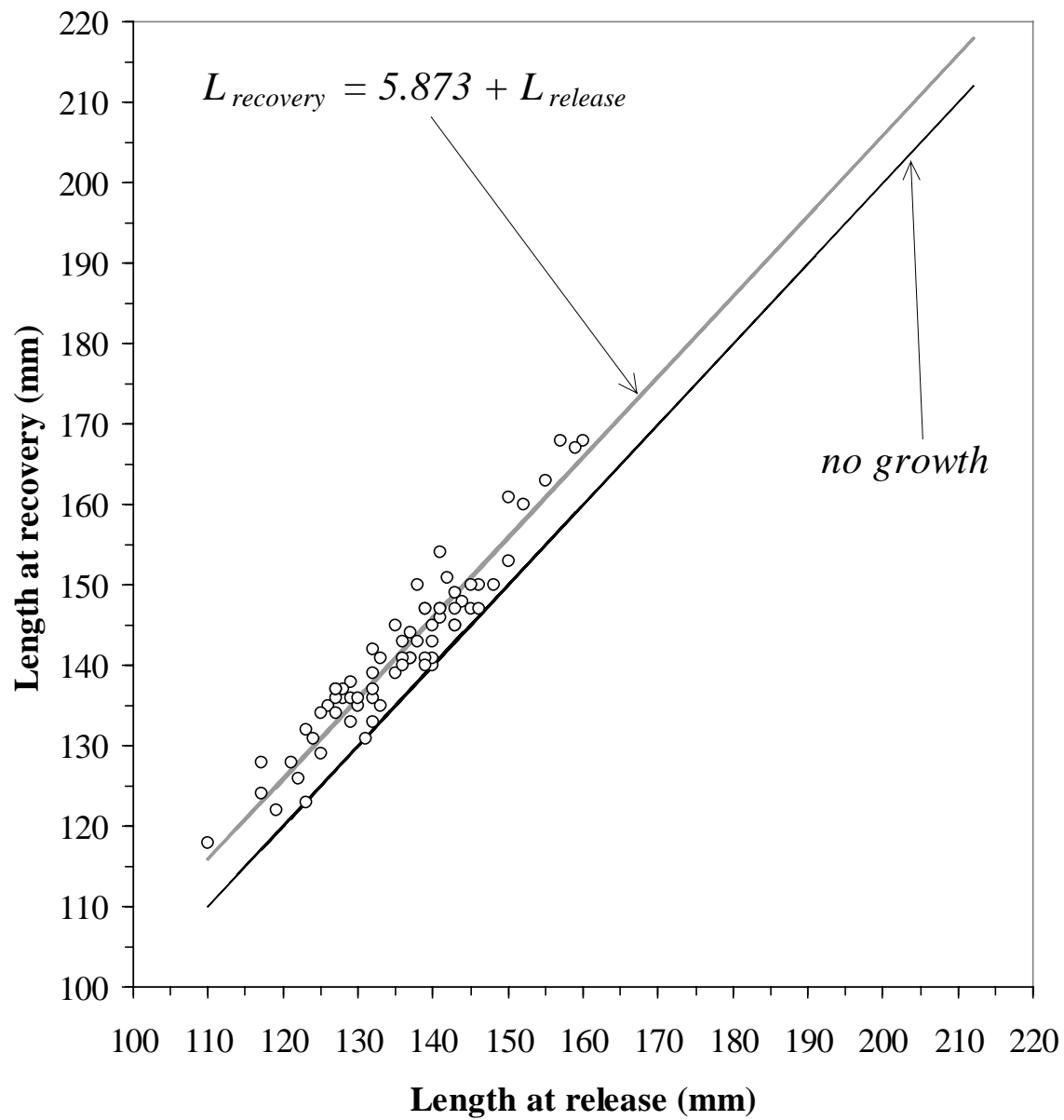
b)

	r^2	0.9071			
	Coefficients	SE	Lower 95%	Upper 95%	
α Intercept	9.606	5.1	-0.567	19.78	
k Slope	0.972	0.037	0.898	1.047	

c)

H_o	Residual SS	<i>df</i>	F	$P.$
$k = 1$	711.86	70	$\frac{(711.86 - 706.34)}{10.24} = 0.539$	0.4654

Figure 8: Walford's line for a sub-sample of 71 fish (mode of travel times $7 \leq TT < 8$ days) from a sample of 373 PIT-tagged hatchery spring chinook, measured in the LGR-LMN reach, in 1994.



The comparison of the distributions for the original 373 release and recovery lengths showed clear differences that can also be attributed to growth. Both the Kolmogorov-Smirnov test (Table 6a) and the one-tail paired t-test for the mean lengths (Table 6b) were highly significant.

4.2 Example 2

The second example is for 43 PIT-tagged wild spring chinook smolt, year-class 1994, that traveled from Grande Ronde River (GRANDR) to Lower Granite Dam (LGR). The travel distance was 98 km. It is very unfortunate that no wild fish was sampled in the LGR-LMN reach in 1994 (Table 2). The distribution of the 43 travel times was somewhat spread, with mean and median considerably larger than those from the previous example (Fig. 9). Moreover, probably due to the small sample size, the distribution appears bi-modal.

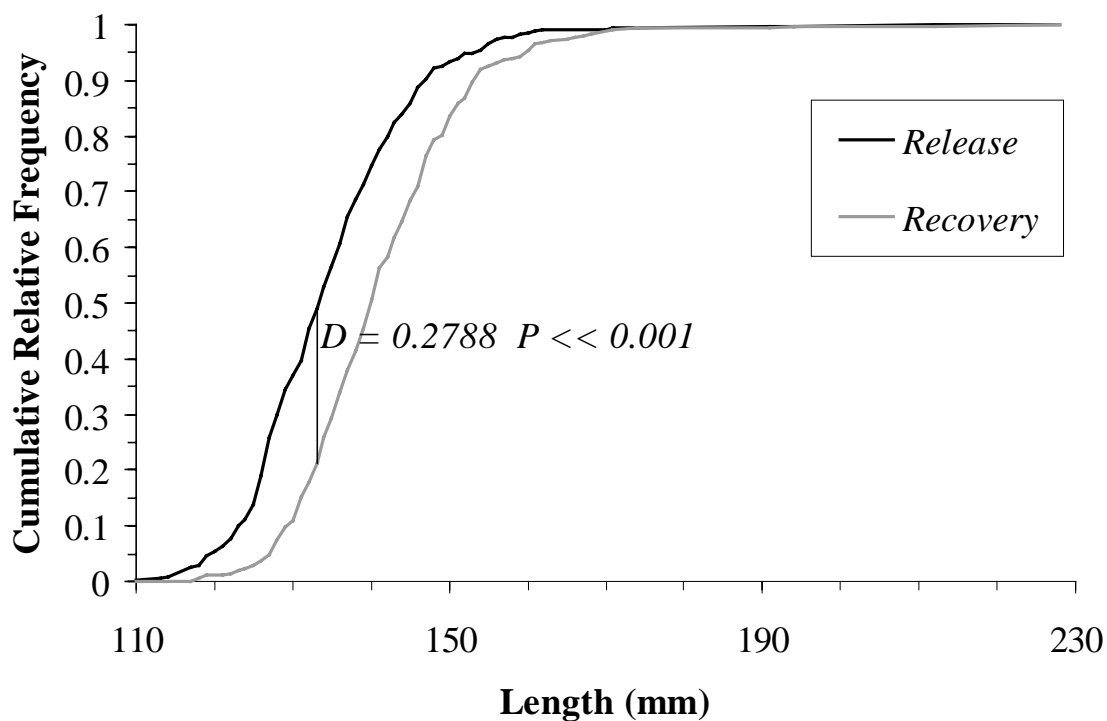
We started by regressing travel time on length at release for the 43 fish in the set, and detected a significant negative correlation (Fig. 10), what implies that the largest fish moved downstream faster than the other tagged fish, and consequently had less time to grow. If we were to use the 43 fish in the analysis of growth, the recovery lengths for larger fish, being smaller than they should be, would affect the estimate of growth and complicate the interpretation of results. To avoid this problem, we inspected the original data set again (Fig. 9). We truncated the distribution of travel times at $TT = 70$ days, and reanalyzed the sub-sample of 36 fish whose travel times were less than 70 days. This sub-sample did not show a significant length effect (Figs. 11); thus, we used this smaller subset ($N = 36$) in the analysis of growth.

The estimated Walford's line had a slope not significantly different from 1 (Table 7). The final line $L_{recovery} = 33.028 + L_{release}$ (Fig. 12) suggests that the wild fish grew some 33 mm during the 43 averaged days of their migration, at an approximate rate of 0.8 mm/day ($\frac{\overline{\Delta L}}{TT} = \frac{33}{43}$).

Finally, the comparison of the distributions for the 36 release and recovery lengths showed clear differences that also suggest the occurrence of growth. Both

Table 6: Comparison of release and recovery lengths for 373 PIT-tagged hatchery spring chinook, measured in the reach LGR-LMN, in 1994, (all travel times $4.5 \leq TT < 27.5$ days). **a)** Cumulative relative frequencies for lengths at release and recovery, and Kolmogorov-Smirnov statistic D , **b)** Sample summaries and paired t-test.

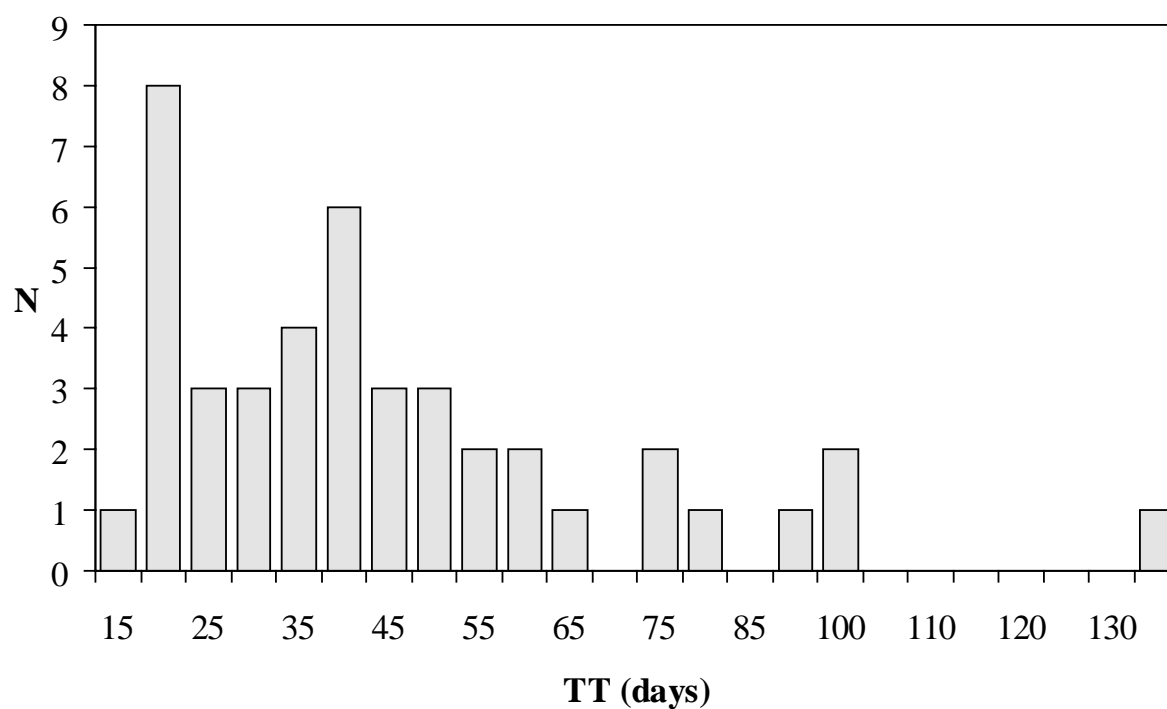
a)



b)

	<i>Length at Release</i>	<i>Length at Recovery</i>
Mean	134.94	141.62
Variance	116.18	121.45
Observations	373	373
Pearson Correlation	0.961	
<i>df</i>	372	
t Stat	-42.043	
P(T<=t) one-tail	1.1E-143	

Figure 9: Distribution of travel times for wild spring chinook, year-class 1994, in the Grande Ronde River-Lower Granite (GRANDR-LGR) reach.



<i>MEAN</i>	<i>42.91</i>
<i>STD. DEV.</i>	<i>25.95</i>
<i>MODE</i>	<i>31</i>
<i>MEDIAN</i>	<i>38.03</i>
<i>25 PERCENTILE</i>	<i>23.62</i>
<i>75 PERCENTILE</i>	<i>51.10</i>

Figure 10: Relationship between travel time and release length for 43 PIT-tagged wild spring chinook, year-class 1994, in Grande Ronde River-Lower Granite (GRANDR-LGR) reach (all travel times included).

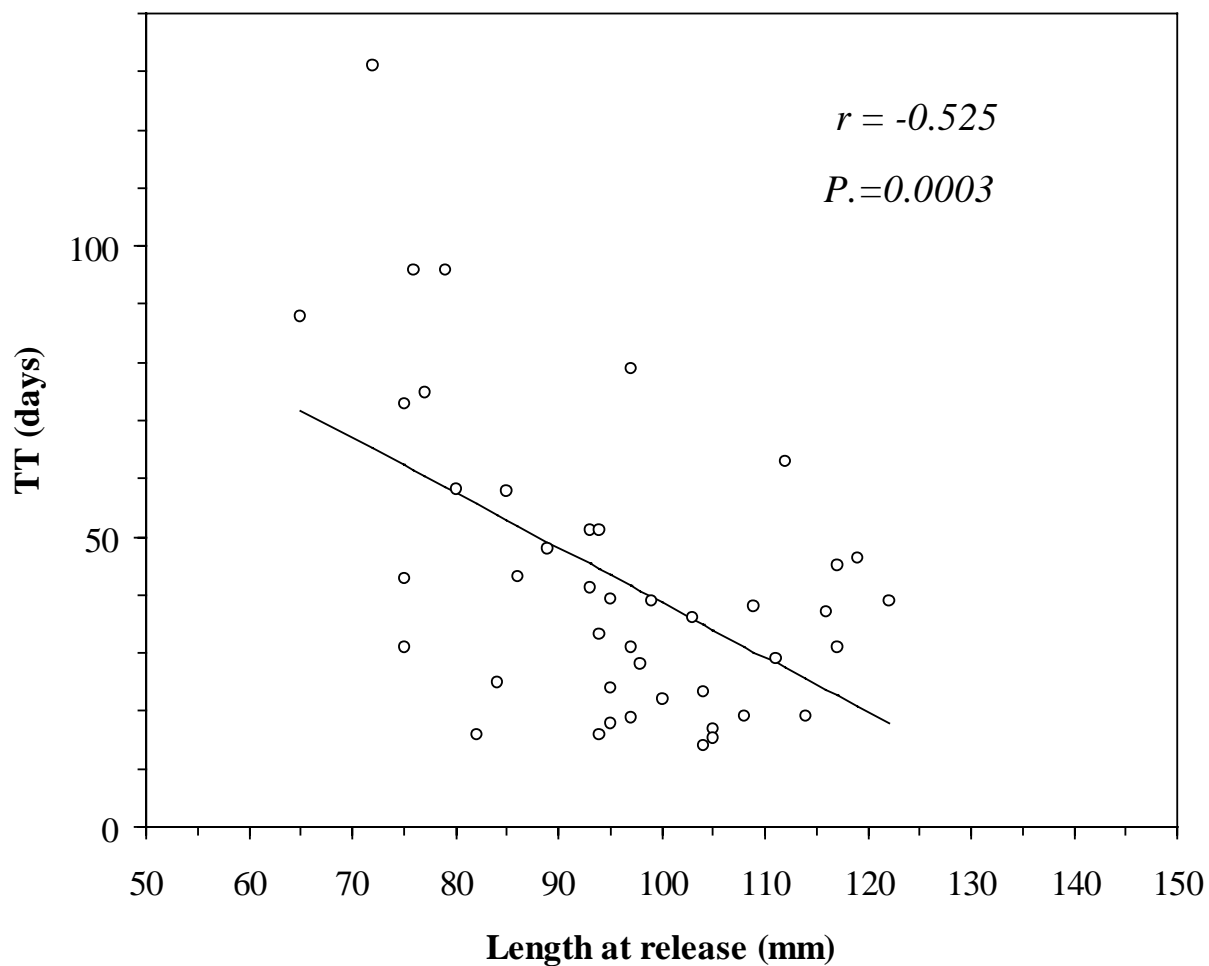


Figure 11: Relationship between travel time and release length for a sub-sample of 36 PIT-tagged wild spring chinook, year-class 1994, in Grande Ronde River-Lower Granite (GRANDR-LGR) reach (travel times of less than 70 days).

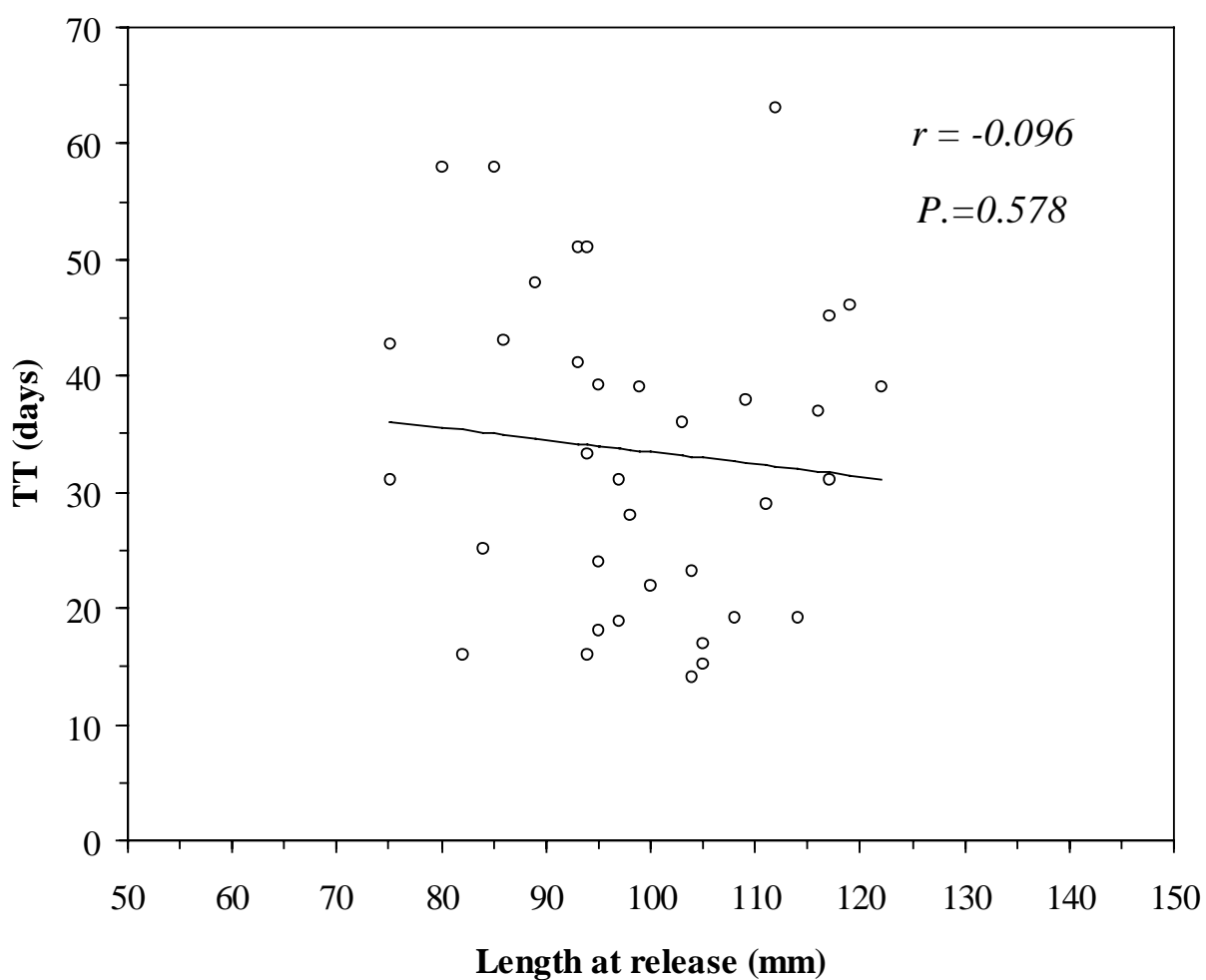


Table 7: Walford's line for a sub-sample of 36 fish (travel times of less than 70 days) from a sample of 43 PIT-tagged wild spring chinook, measured in the GRANDR-LGR reach, in 1994. **a)** ANOVA table, **b)** Coefficient of determination (r^2), regression coefficients, standard errors (SE) and 95% confidence intervals, and **c)** F-ratio test for model $L_{recovery} = \alpha + L_{release}$ (growth without effect of length at release).

a)

	<i>df</i>	SS	MS	F	P-value
Regression	1	3373.27	3373.270	10.705	0.002
Residual	34	10713.48	315.102		
Total	35	14086.75			

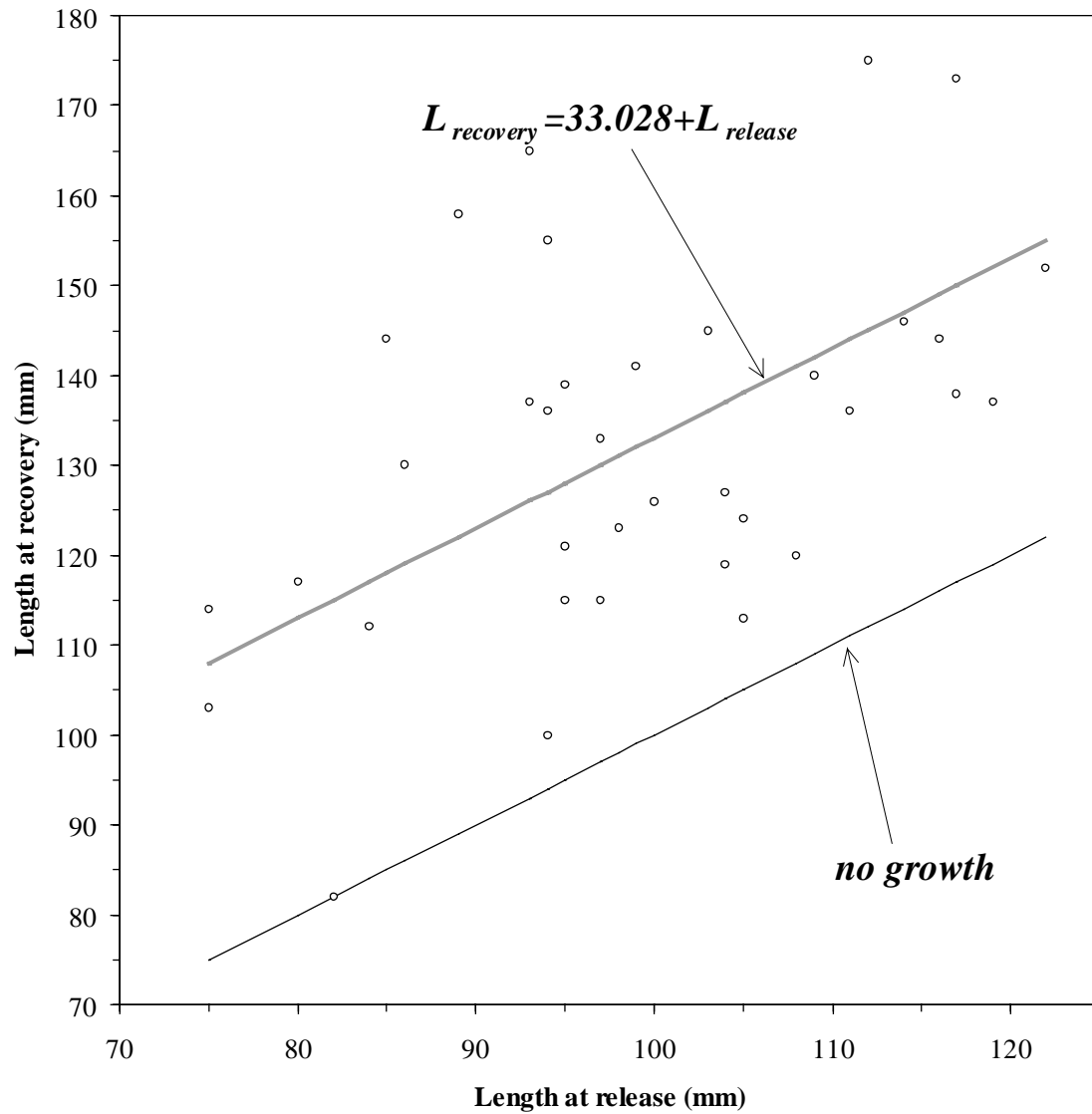
b)

r^2	0.2395			
	Coefficients	SE	Lower 95%	Upper 95%
α Intercept	53.937	24.067	5.028	102.846
k Slope	0.789	0.241	0.299	1.279

c)

H_o	Residual SS	<i>df</i>	F	$P.$
$k = 1$	10954.97	35	$\frac{(10954.97 - 10713.48)}{315.10} = 0.766$	0.3875

Figure 12: Walford's line for a sub-sample of 36 fish (travel times of less than 70 days) from a sample of 43 PIT-tagged wild spring chinook, measured in the GRANDR-LGR reach, in 1994.



the Kolmogorov-Smirnov test (Table 8a) and the one-tail paired t-test for the mean lengths (Table 8b) were highly significant.

4.3 Comparison of Growth between Samples

The previous applications of Walford's lines, Kolmogorov-Smirnov tests and one-tail paired t-tests have shown the occurrence of in-river growth for hatchery spring chinook migrating from LGR to LMN, and for wild fish migrating from GRANDR to LGR. Moreover, we have inferred that the hatchery fish was growing at an approximate rate of 0.6 mm/day, while the wild fish was growing at the apparently faster rate of 0.8 mm/day. However, the rather strict condition of a constant travel time within a sample, that the three methods impose, and the somewhat opportunistic¹ nature of the present growth analysis prevented a statistically formal comparison of growth between samples. We circumvented the problem by calculating the growth rate,

$$G_i = \frac{(L_{recovery} - L_{release})_i}{TT_i}, \text{ for both samples, and minimizing linear model (6).}$$

First, we fitted model M_0 that assumes that the growth rate of each sample can be expressed as a distinct linear function of day of release, length at release and fish speed. The fit predicted that:

$$\hat{G} = 0.325 - 2.979I + 0.009D + 0.017DI - 0.005L + 0.005LI - 0.066S + 0.101SI ,$$

or expressed in other terms:

$$\hat{G} = 0.325 + 0.009D - 0.005L - 0.066S, \text{ for the sample of wild fish,}$$

and

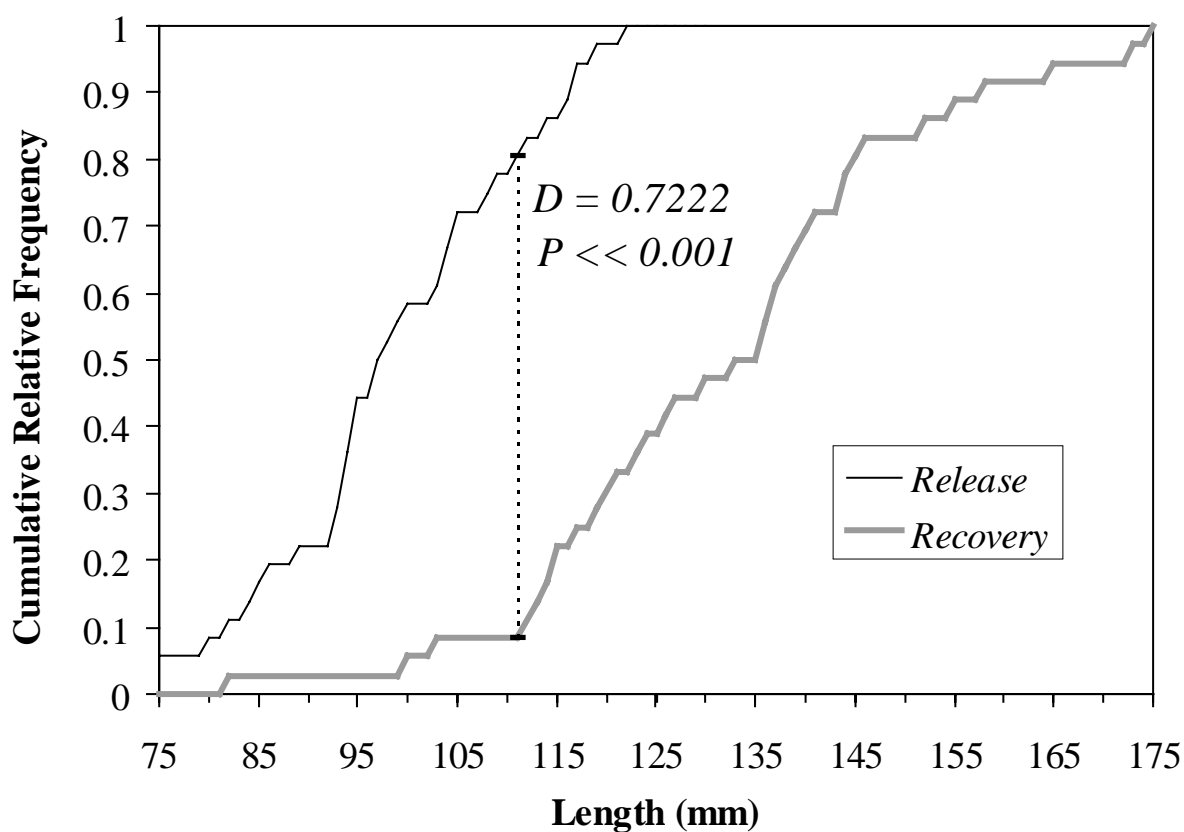
$$\hat{G} = -2.654 + 0.025D - 0.0004L + 0.035S, \text{ for the hatchery fish.}$$

Eight other models (M_1 - M_8) were also fitted to the data (Table 9). Their fits were tested by series

¹ Most of the PIT-tag releases of 1994, 1995 and 1996 had the primary objective of estimation survival instead of growth.

Table 8: Comparison of release and recovery lengths for a sub-sample of 36 fish (travel times of less than 70 days) from an original sample of 43 PIT-tagged wild 1994 spring chinook, measured in the GRANDR-LGR reach. **a)** Cumulative relative frequencies for lengths at release and recovery, and Kolmogorov-Smirnov statistic D , **b)** Sample summaries and paired t-test.

a)



b)

	<i>Length at Release</i>	<i>Length at Recovery</i>
Mean	99.06	132.08
Variance	154.85	402.48
Observations	36	36
Pearson Correlation	0.489	
<i>df</i>	35	
t Stat	-11.201	
P(T<=t) one-tail	2.009E-13	

Table 9: Regression coefficients ($\hat{\alpha}_i$), residual sum of squares (RSS) and degrees of freedom (df) for various linear models (M_i) fitted to the growth rates of two samples of PIT-tagged hatchery spring chinook. The samples consisted of 373 PIT-tagged hatchery 1994 spring chinook, measured in the LGR-LMN reach, and 43 wild 1994 spring chinook, measured in the GRANDR-

LGR reach. Growth rates were calculated as $G = \frac{(L_{recovery} - L_{release})}{TT}$ (mm/day). There were

four model variables. I was an indicator variable that took value 0 when the sampled fish came from the wild-fish sample, and 1, otherwise. D was the day when the tagged fish was released at the lower reach boundary, expressed as a number ranging from 1 to 365. L was the length at

release, in mm, and S was the fish speed, in km/day, measured as $S = \frac{d}{TT}$, with d equal to 106 km

for the hatchery fish and 98 km for the wild fish. TT is the fish travel time, measured in days.

Empty cells indicate that the parameter α_i was assumed equal to zero.

Models	$\hat{\alpha}_0$	I $\hat{\alpha}_1$	D $\hat{\alpha}_2$	$D \times I$ $\hat{\alpha}_3$	L $\hat{\alpha}_4$	$L \times I$ $\hat{\alpha}_5$	S $\hat{\alpha}_6$	$S \times I$ $\hat{\alpha}_7$	RSS	df
M_0	0.325	-2.979	0.009	0.017	-0.005	0.005	-0.066	0.101	41.725	408
M_1	-0.297		0.010		-0.004		0.033		45.079	412
M_2	0.099	-1.270	0.013		-0.009	0.008	-0.091	0.130	42.813	409
M_3	0.141	-2.703	0.007	0.019	-0.001		-0.067	0.102	41.834	409
M_4	0.541	-3.231	0.005	0.021	-0.005	0.005	0.032		42.567	409
M_5	0.100	-2.823	0.007	0.019			-0.067	0.102	41.877	410
M_6	-0.389	-0.624	0.011				-0.099	0.138	43.353	411
M_7	0.306	-3.062	0.004	0.023			0.032		42.734	411
M_8	0.240	-2.963	0.005	0.022				0.035	42.258	411

of F-ratio tests (Table 10) to find whether two distinct regression lines were needed. Model M_1 that assumes a common regression line for both samples was rejected ($P = 2.279 \times 10^{-6}$). However, for an α -level of 0.05, the simpler model M_8 was not ($P = 0.0541$, Table 10). Thus, we selected M_8 to describe the growth rate in the two samples. Model M_8 estimates growth rate as:

$$\hat{G} = 0.240 - 2.963I + 0.005D + 0.022DI + 0.035SI,$$

or:

$$\hat{G} = 0.240 + 0.005D, \text{ for the sample of wild fish,}$$

and

$$\hat{G} = -2.723 + 0.026D + 0.035S, \text{ for the hatchery fish.}$$

The goodness-of-fit of model M_8 can be observed in Figure 13.

Figure 14 shows the growth rates predicted by model M_8 for the hatchery and wild fish, as function of release day with a constant fish speed (Fig. 14a), and as function of fish speed for fixed release days (Fig. 14b). From the predicted growth rates (\hat{G}), we derived expected lengths-at-recovery ($\hat{L}_{recovery}$) as: $\hat{L}_{recovery} = \hat{G} \times TT + L_x = (\hat{\alpha}_0 + \hat{\alpha}_1 D_x + \hat{\alpha}_2 S_x) \times TT + L_x$, where the $\hat{\alpha}_i$ are the parameter estimates for model M_8 , and D_x , S_x and L_x are fixed or constant release day, fish speed and length-at-release, respectively. Figure 15 shows the increase in length-at-recovery predicted by the model for increasing travel times. It was assumed that 1) the hatchery fish were released on 24 April, at constant lengths of 134.9 mm, 2) the hatchery fish traveled at a constant speed of 11.583 km/day, and 3) the wild fish were released on 27 May, at lengths of 95.5 mm. The constant values D_x , S_x and L_x used to draw the lines in Figures 14 and 15 were the average release days, speeds and lengths-at-release from each sample. However, other values could be used to further explore the predictions of model M_8 .

Table 10: F-ratio tests for selection of a parsimonious model fitted to growth rates,

$G = \frac{(L_{recovery} - L_{release})}{TT}$ (mm/day), observed in the sample of 373 PIT-tagged hatchery spring chinook, measured in the LGR-LMN reach, and the sample of 43 wild spring chinook, measured in the GRANDR-LGR reach, in 1994. See Table 9 for parameter estimates and variable names.

	MODEL	TEST	F	P-value
M_0	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_4 L + \alpha_5 LI + \alpha_6 S + \alpha_7 SI$			
M_1	$G = \alpha_0 + \alpha_2 D + \alpha_4 L + \alpha_6 S$	$\alpha_1 = \alpha_3 =$ $\alpha_4 = \alpha_7 =$ 0	8.201	0.0000
M_2	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_4 L + \alpha_5 LI + \alpha_6 S + \alpha_7 SI$	$\alpha_3 = 0$	10.641	0.0012
M_3	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_4 L + \alpha_6 S + \alpha_7 SI$	$\alpha_5 = 0$	1.070	0.3016
M_4	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_4 L + \alpha_5 LI + \alpha_6 S$	$\alpha_7 = 0$	8.238	0.0043
M_3	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_4 L + \alpha_6 S + \alpha_7 SI$			
M_5	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_6 S + \alpha_7 SI$	$\alpha_4 = 0$	0.417	0.5190
M_5	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_6 S + \alpha_7 SI$			
M_6	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_6 S + \alpha_7 SI$	$\alpha_3 = 0$	14.456	0.0002
M_7	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_6 S$	$\alpha_7 = 0$	8.399	0.0040
M_8	$G = \alpha_0 + \alpha_1 I + \alpha_2 D + \alpha_3 DI + \alpha_7 SI$	$\alpha_6 = 0$	3.732	0.0541

Figure 13: Residual plot for model M_8 fitted to the sample of 373 PIT-tagged hatchery spring chinook, measured in the LGR-LMN reach, and the sample of 43 wild spring chinook, measured in the GRANDR-LGR reach. Diagonal line indicates a “perfect” fit.

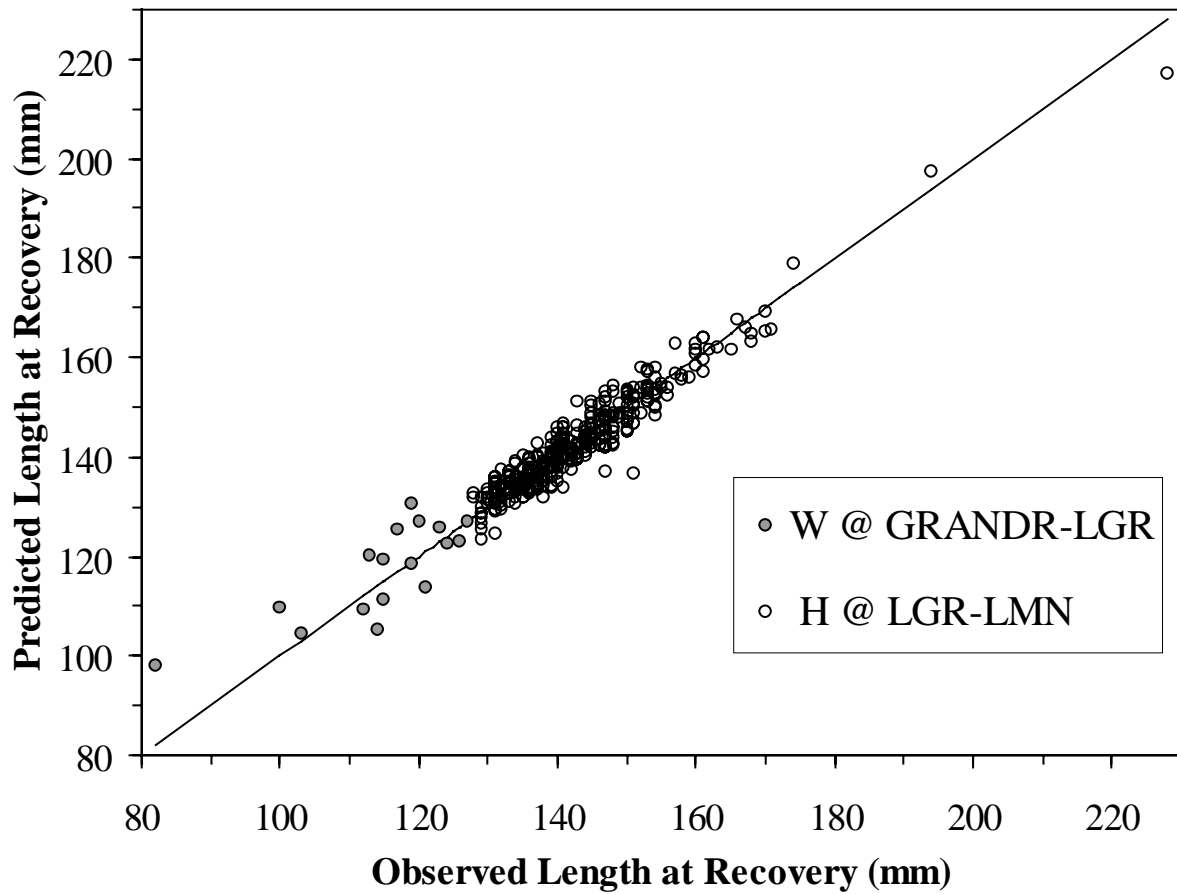


Figure 14: Growth rate G as function of (a) release day and (b) fish speed. Open squares indicate observations of hatchery spring chinook in the LGR-LMN reach, and solid circles are observations of wild spring chinook in the GRANDR-LGR reach during 1994. Lines indicate growth rates predicted by model M_8 for the sample of wild fish (grey line) and for that of hatchery fish (black line). Predicted lines were calculated using the coefficients in Table 9, and assuming a hatchery-fish average speed of 11.583 km/day (a), and releases on 24 April and 27 May, for the hatchery and wild fish, respectively (b).

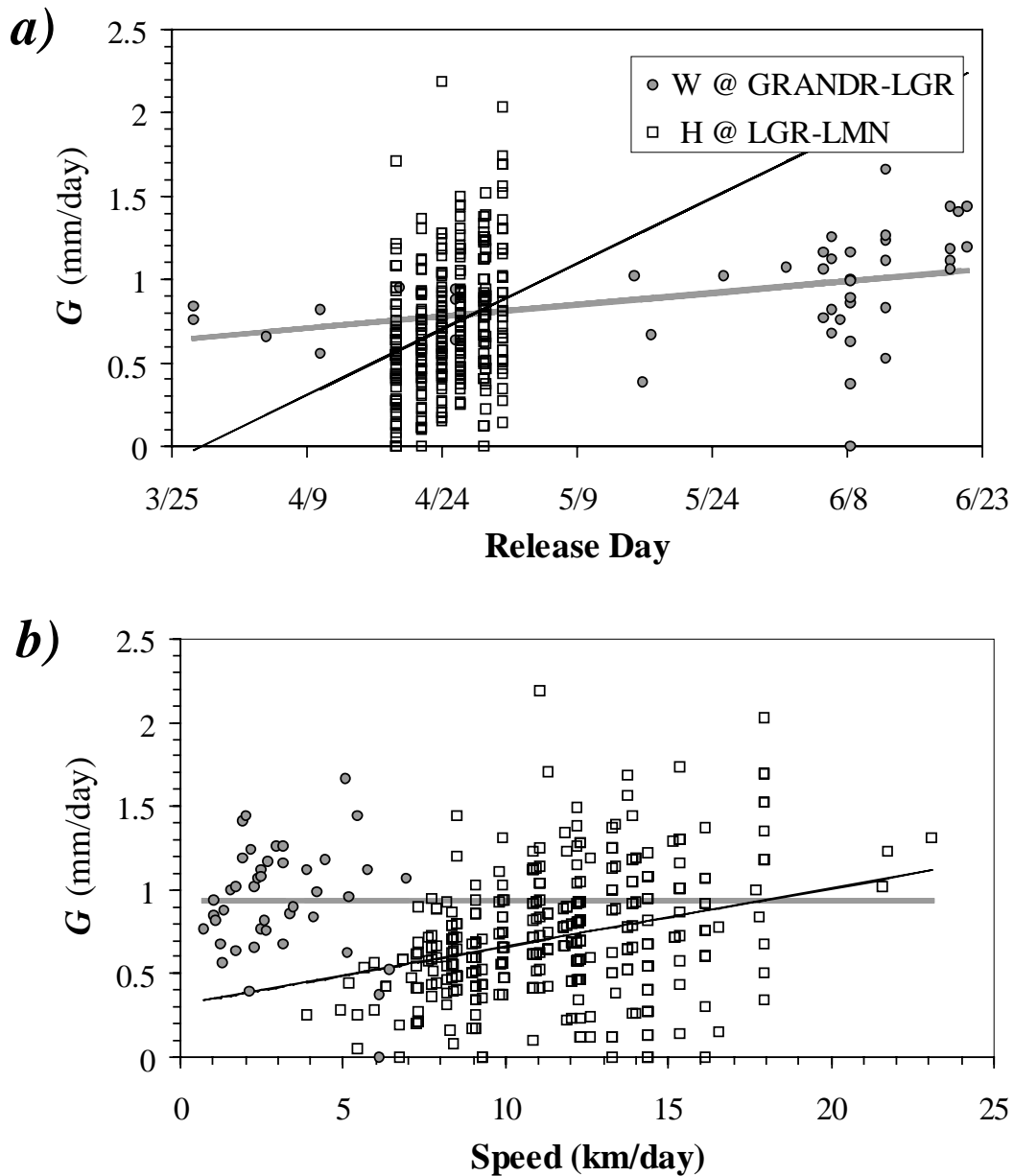
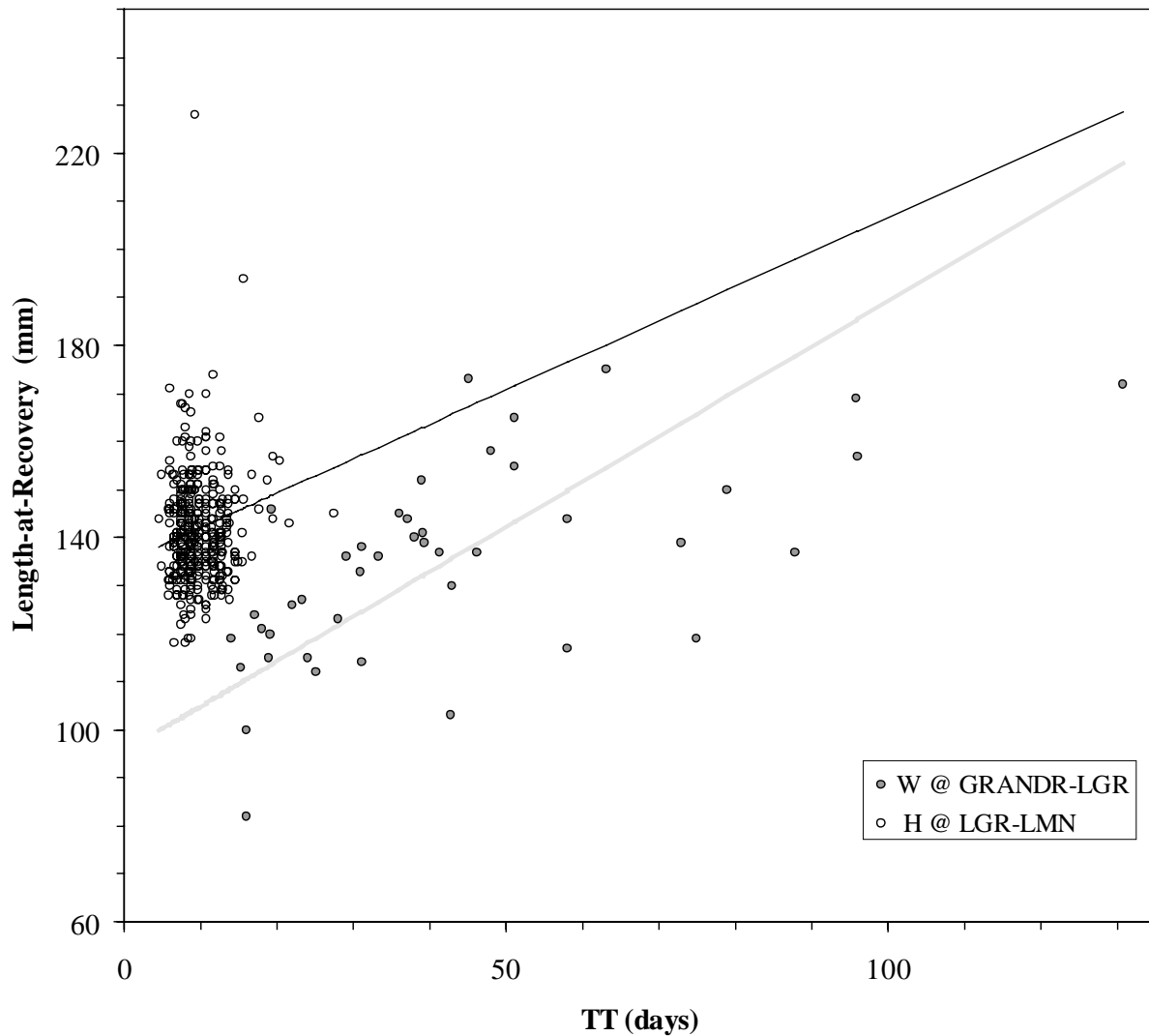


Figure 15: Length-at-recovery as function of travel time. Open circles indicate observations of hatchery spring chinook in the LGR-LMN reach, and solid circles are observations of wild spring chinook in the GRANDR-LGR reach during 1994. Lines indicate recovery lengths predicted by model M_8 for the sample of wild fish (grey line) and for that of hatchery fish (black line). Predicted lines were calculated using the coefficients in Table 9, and assuming that the hatchery fish were released on 24 April, with a constant initial length of 134.9 mm, and traveled at constant speed of 11.583 km/day, and that the wild fish were released on 27 May, with a constant initial length of 95.5 mm.



5. DISCUSSION

In this report we presented three simple methods; Walford's lines, Kolmogorov-Smirnov tests and one-tail paired t-tests, that use lengths of release and recovery of PIT-tagged fish to answer whether the fish in the sample grew during the tagging period. As with many other analyses based on marked individuals, these methods assume that tags do not retard growth. This assumption appears to hold for PIT-tagged juvenile salmonids, for which only a slight, but not statistically significant, depression of growth has been reported during the first 20 days after tagging (Prentice et al., 1990).

Walford's lines, Kolmogorov-Smirnov tests, and one-tail paired t-tests can certainly answer whether the PIT-tagged fish in the sample grew between release and detection times. However, they answer this simple question in different ways. With the Kolmogorov-Smirnov test, growth between release and detection times is confirmed if the hypothesis that the distributions of release and recovery lengths are equal is rejected at a given α level. The t-test assumes that the difference between recovery and release lengths d_i is normally distributed. Growth between release and detection times is confirmed when the hypothesis that $d_i \leq 0$ is rejected.

Walford's lines actually estimate the growth the two other methods simply detect. Walford's lines express growth as a linear relationship between recovery and release lengths. Growth between release and detection times is confirmed when the hypothesis that the line is equal to the line $\hat{L}_{recovery} = 0 + 1 \times L_{release}$ is rejected. This test is easily performed in an ANOVA setup. Its linear form makes Walford's lines an interesting way to express growth. Not only the slope coefficient k can be tested for a significant effect of release length, but also lines obtained with different datasets can be compared, the extent and type of the comparison being limited by the quality of the data. For example, lines obtained for hatchery and wild chinook of a same year class and run, traveling during the same time, in different locations, could be tested for significant differences among intercepts and slope coefficients k , attributable to rear-type or habitat (location). Similarly, lines obtained for different runs and year classes could be compared.

Determining growth from tagged data require homogeneous samples of adequate size ($N \geq 30$ fish). All tagged fish in the samples must be of about the same age and of the same origin. Moreover, they must also be released at about the same time (e.g., month or season) to avoid biased estimates. Fish marked months apart may grow at very different seasonal rates during the tagged period. Thus, growth estimates may be biased and difficult to interpret. Moreover, if the lengths at time of release and recovery of the individual fish in the sample are not measured over similar periods of times (travel times), estimates of growth rates may be biased. In the present report, we have sketched a three-step protocol (identification of reaches with large sample size, inspection of travel-time distributions, and assessment of the relationship between travel time and release length) for the initial selection of PIT-tagged data that may constitute adequate samples for the study of growth.

The application of Walford's lines, Kolmogorov-Smirnov tests and one-tail paired t-tests to two samples of PIT-tagged spring chinook, one of hatchery-reared releases and one of wild releases, have shown the occurrence of in-river growth in both cases. The hatchery fish grew on average some 6 mm over a period of around 10 days, while the wild fish grew some 33 mm during an average migration time of 43 days. However, the rather strict condition of a constant travel time within a sample, that the three methods impose to avoid biased estimates, prevented a statistically formal, direct comparison of growth between the two samples. To make possible a comparison of sorts, we defined individual growth rates (\hat{G}) as the difference between the observed lengths at release and recovery, divided by the travel time of each fish in the samples. The calculated growth rates were fitted to a linear model with three predictor variables: the release day (D), the length at release, and the fish average speed (S), calculated as the travel distance over the individual travel times. After a series of F-ratio tests, we determined that the wild and hatchery fish in our examples grew at different rates: $\hat{G} = 0.240 + 0.005D$ for the wild fish, and $\hat{G} = -2.723 + 0.026D + 0.035S$ for the hatchery fish.

Until PIT-tag experiments designed to assess growth under particular circumstances are performed, Walford's lines, Kolmogorov-Smirnov tests or one-tail paired t-tests may be applied to samples from the current PIT-tag data base. However, these samples should not be selected solely on the basis of the particular criterion of interest (e.g., reared type, time and locale of

migration, size at release, site of origin, etc). Careful attention must be paid to the inspection of the travel-time distribution and the correlation between travel time and release length of each potential sample to avoid bias in the analysis of growth. Once that growth has been detected for a sufficient number of adequately selected samples, linear modeling may be used to compare between-samples growth rates.

6. REFERENCES

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7. APPENDIX: Names of sampling locations

Location code	Location name	Location code	Location name
BEARVC	Bear Valley Creek	LGS	Little Goose dam
BIGC	Big Creek	LMN	Lower Monumental dam
BIGFLC	Big Flat Creek	LOLOC	Lolo Creek
CAMASC	Camas Creek	LOOH	Looking-glass hatchery
CATHEC	Catherine Creek	LOOKGC	Looking-glass Creek
CFCTRP	Crooked Fork Creek trap	LOSTIR	Lostine River
CHAMWF	Chamberlain Creek west fork	MARSHC	Marsh Creek
CLEARC	Clear Creek	MARTRP	Marsh Creek trap
CLWTRP	Clearwater trap	MCN	McNary dam
CROOKC	Crooked Fork Creek	PAOOC	Papoose Creek
CROOR	Crooked River	PETEKC	Pete King Creek
CROTRP	Crooked River trap	POWP	Powell rearing plant
DWOR	Dworshak hatchery	RAPH	Rapid River hatchery
ELKC	Elk Creek	REDP	Red River rearing plant
ENTH	Entiat hatchery	REDTRP	Red River trap
FRENCC	Frenchman Creek	RIS	Rock Island dam
GRANDR	Grande Ronde River	SALR	Salmon River
HERDC	Herd Creek	SALTRP	Salmon River trap
IMNAHW	Imnaha River weir	SAWT	Sawtooth hatchery
IMNTRP	Imnaha trap	SAWTRP	Sawtooth trap
JDA	John Day dam	SNAKER	Snake River
KOOS	Kooskia hatchery	SNKTRP	Snake River trap
LAKEC	Lake Creek	SQUAWC	Squaw Creek
LEAV	Leavenworth hatchery	WHITSC	White Sand Creek
LEMHIW	Lemhi weir	WINT	Winthrop hatchery
LGR	Lower Granite dam		